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September 2, 2004, 00:17:05 ; Search time 7415 Seconds
(without alignments)
11024.270 Million cell updates/sec 6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 gb_ba:*
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gb_pi: Minimum DB seq length: 0 Maximum DB seq length: 200000000 GenEmb1:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		A80126 A.	AV072174	AX384394	AX473364	AY0965	ABULZ/ A.Challana Al031804 Arabidon	AL161582	Z83320 A	AF3 /596 / AF4 06703	AF406697	AF375966	AK067939	AK069994 AF406698	AF406702	AK109849	AK061393	AX104 / 13 AX506642	BT008422	AY096548	AF353094 AY072175	AY099854	AF406700	AX507459 AX507459 Sequence	A1052368 AX412914	90000E	AY056796	AF375964	AKIO48	AK07046	AF40670	AX50621	AY14201	AY0581	AK07054	AF173816 Arabidop	AY050459 Arabidop	ALIGNMENTS		1886 bp mRNA linear PLN 02-MAR-19			(thale cress)	Strentonhyta. Embrychyty	borrepropulta, amoijopnita, rracmeopnita, sutta, endicotyledons; core endicots;	100000000000000000000000000000000000000	Rook, F., Weisbeek, P. and Smeekens, S.
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Quaddylieg,N.E.
Direct Submission
Submitted (11-UUL-1994) N.E. Quaedylieg, University of Utrecht,
Dept of Molecular Cell Biology, Padualaan 8, 3584 CH Utrecht,
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1140 1140 CCGAGTCAGGAGCTGCTAGTTCAGCCTTT 1020 1080 1080 ATTGCGTAGATGAGATTCATACGGTTATA 1200 AGAGAATCTGCAAGAAGATAATCTCTATG 1320 ACTCAAGAAACCTCTATGTTCCACCAGCAT 1380 360 420 480 480 540 540 009 660 099 720 720 840 840 960 360 420 600 900 900 960 TTAGTTCTCTGGATAATGTCATGACTAAC |||||||||||||||||||| TTAGTTCTCTGGATAATGTCATGACTAAC CAAGAGAATTCAACTTCATTCTCAACA CTCATCCTCCACTTCATCCTTTGGAT GTCTTTGTGCAGCTACAAGATTAGCCTCA CTGTTCAAGAAATACTATCTCATTTCGCC TTGATGGTGATTCTAATAACTCGGAGGGG |||||||||||||||||||| TTGATGGTGATTCTAATAACTCGGAGGGG CTAATAACGTTGTTACTCAAGGTTTCTCT TAGAAGCAAAGAAACCCATCTCTTGGAT |||||||||||||||||| TAGAAGCAAAGAAAACCCATCTCTTGGAT CTAATAACGTTGTTACTCAAGGTTTCTCT

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Query Match 97.9%; Score 1846; DB Best Local Similarity 99.4%; Pred. No. 0; Matches 1863; Conservative 0; Mismatches
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Syamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninot, P., Chen, H., Cheuk, R., Haysahsaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Full Length cDNA Clones

Arabidopsis Full Length cDNA Clones

Lobases 1 to 2277)

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, B., Dale, J.M., Dondera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Mu, H.C., Yamamura, Y., Yu, G., Bowser, L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Shinozaki, K., Baytin, Schi, M., Shinn, P., Southwick, A., Saki, M., Seki, M., Shinn, P., Southwick, A., Shinn, P., Southwick, A., Bohin, S., Bohin, Expression Center, 800 Buchanan
                                                          1440
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                                                                                                                 1381 recententeaceacencaaccaaceaacaaccareacaringaacacereaaccacearing 1440
                                                                                                                                                                        1441 cergagaaarererreegerreracegaarregarerreeaaacrreerreerree 1500
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GGATCTGTATTGGAGAGAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCAT 1380
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eparatophyta, Wagnoliophyta, eudicocyledons, core eudicocs,
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
1 (bases 1 to 2277)
                                                          TGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTG
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KEYWORDS
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                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Chan, M., Chang, C.H., Chang, C.H., Dale, J.M., Deng, J.M., Codera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Greuk, K., Jones, T., Karlinn-Neuwann, G., Kim, C., Lam, B., Lin, J., Myranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert."
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/chromosome="4"
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/gene="At4g32980"
/note="compared to
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1484	RESULT 4 AX384394 LOCUG DEFINITION Sequence 3 from Patent W00214524. ACCESSION AX384394 AX384
1 ATTACTIVITAMANICITICCIATITICINAL CINCINAL CONTINUACIONAL CONTINU	840 AGGCAAGCTTCTTGCAGCAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTC 899 1244 AGAGCAAGCTTCTTGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTC 1303 900 TCAACTTTTGCAAAATACCTTCTTCAAGAAATACTTTCGC 959 1304 TCAACTTATTTGGCTAAAATACCTTCATTCAAGAAATACTATTCGC 959 1304 TCAACTTATTTGGCTAAAATACTTCACTTCAAGAAATACTATTCGC 1363 960 GGCATACTCGCTCGAATATTCATCTCACTTCACTTCAAGAAATACTATTCGC 1363 960 GGCATACTCGCTCGATTATTCATCTCTCGAGGAACCGAGTCAGGAGCTGCTATTCAGCTT 1019 1364 GGCATACTCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTT 1423 1020 TACTTCACGTTTTGAGAATATAACTGGAGGAACCGAGTCAGGAGTTCTAATAACTCGAGGC 1079 1424 TACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGC 1483 1080 GGGTTTCGGATTTCAAAGGAGCATTAGAAAAAACCCCATCTTGGA 1139

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)391699 hotce="unnamed protein product; Beta-lactamase gene AmoR)"	5525 CTCAACTTATATTTGGCTCAAAATACCTTCACTCTGTTCAAGAAATACTATCTCATTTGG 558
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X XXEE = "REMTERMEN. (2D28571" (b. XIVEE = "REMTERMEN. (2D28571" (r. Inc.)	Qy 1019 TTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGG 1078
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29414920 49216400 7note="AtH1 gene from Arabidopsis thaliana"	OY 1139 ATCTTCAAATGGGGATGATCGATAATCCATTGCGTAGATGAGATTCATACGGTTA 1198
64016672 /note="Poly-A signal from the nopaline synthetase gene from Agrobacteriu m tumefaciens" 74348084	Qy 1199 TATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACGGGTTTGCCCTCC 1258
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78.3%; Score 1476; DB 6; Length 9359; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1319 TGGGATCTGTATTGGAGAGAGAGACAAGACTCAAGAAACCTCTATGTTCCACCAGC 137
CTCTGGATAATGTCAT	Qy 1379 ATTGCCTTCTTCAGCAGCTCAAAGCAAAGAACCATCAGATTTGGAGACCTCAACGAGGTT 1438
TCTCAA 41	149
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TCAATTCTATGCTGACTAACAAATACTTATCATCTCTCCACGGTCTATCGATGTTCAAG 538	1559 TATCAAACTGGTTTATAAATGCGCGGGTTAGGGAGGCCATGATGATGAAGAATGT 161
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argargatticccgittctaatticgaataaagaaagaagatgactticattgagicttg 778 	
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CAGAGCAAGCTTCTTGCAGCAGGAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCT 898	SOURCE SYNCHELIC CONSTRUCT ORGANISM SYNCHELIC CONSTRUCT

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AY096513 1453 bp mRNA linear PLN 18-SEP-2002 (Atabidopsis thaliana putative homeobox gene ATH1 protein (Atag12980) mRNA, complete cds.

NAV096513 GI:20465954
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Tamaga, X., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldemith, A.D., Lee, J.M., Condera, C.S., Quach, H.L., Carninci, P., Chen, H., Chang, J., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
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                                             Inhibition of generative propagation in genetically modified grasses

Inhibition of generative propagation in genetically modified grasses

In patent: WO 0214486-A 1 21-FEB-2002;

Advanta Seeds B.V. (NL)

Advanta Seeds B.V. (NL)

Coration/Qualifiers

1. 9359

/organism="synthetic construct"
//mol type="unassigned DNA"
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Location/Qualifiers
              Palm, C.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, K., Jones, T., Karlin-Neumann, G., Kim, C., Lad, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Sakurai,T., Satcu,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Arabidopsis Open Reading Frame (ORF) Clones
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	Db 1141 GAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCCTTC	Oy 1504 AAAGATICGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCA 1563	OY 1564 AACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCG 1623	QY 1624 GANATGAACAGAAGCTCAATAACAGTCACATTCAACCCAACGGACCAACTCTTCGA 1683	QY 1684 AIGCCAAAAICTGTTAIGAIGAGCCAAGCAAIGCATAAATAAGACAACAATTGTGTTTAC 1743 Db 1381 AIGCCAAAAICTGTIAIGAIGAGCAAGCAATGCATAAATAAGACAACAATGGTTTAC 1440	Qy 1744 CAACTITGIGATA 1756	RESULT 7	-	ACCESSION X80127 VERSION X80127.1 GI:685235 KEYNORDS HI gene Arabitana (thale access)	MSIN	Spermatophyta; Magnollophyta; eudlocyledons; core eudlocts; rosids; eurosids; II; Brassicales; Brassicaceae; Arabidopsis.	AUTHORS Quaedvlieg, N., Dockx, J., Rook, F., Weisbeek, P. and Smeekens, S. TILLE The homeobox gene ATH1 of Arabidopsis is derepressed in the photomorphogenic mutants copi and detl		AUTHORS Quaedvileg, N.B. TITLE Direct Submission JONRNAL Submitted (11-JUL-1994) N.B. Quaedvileg. University of Utrecht.	Dept of Molecular Cell Biology, Padualaan 8, 3584 CH Utree NETHERLANDS	urce	/curryar-colombar/ /db_xref="taxon:3702" /tissue_type="rosette leaves" /clone_lib="H(lambda_ZAP) and H1pr(lambda-Gem)"	Join (2481. 2585,2598. 3332,3425. 3765,3858. 3921, Join (2481. 2585,2598. 3332,3425. 3765,3858. 3921,	4325. 4488) / 4326. 4488) / 5000n scart=1 / protein_id="CAC51426.1"	/ CD_XXEI="G1: 1.2X159.13" / translation="MDNNNNTFESLDNVMTNQNPLLMDF1PSREDSTMLPWTIRS DPLONGGF0IFENSMLTNXTSSSERSIDNQDNRNVBFWAPPPPPPPPLHPLDHLRHYDD SSNNWMGFEANSERQAFSGVVGPSEPMMSTFGEEDFPFLISNKRNNELSISLASDVSD

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SGLKNPQTTGTTLTHLIKPEPELDHQFIDIDESNVANPAKARSKRSRGAASTWASRLL
SGLKNPQTTGTTGTTLTHLIKPEPELDHQFIDIDESNVANPAKARSKRSRGAASTWASRLL
STABDSETNPKKQRVKSQPPAGDPAGDMDVDCGESGGGRRCLHCATEKTPQWRTGPMGPK
TLCMACGTRYKSGELVPEXTRASSPFFVWAHSNSHRKVWELRRQKEWRDEHLLSQLR
CENLLMDIRSNGEDFLMHNNTNHVAPPFRHLI"
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/gene="AP4932900"
complement (join(10392. .10683,10773. .10809,10882. .10942,
11225. .11425,11998. .12039))
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contains EST gb:AA041075, AI994034.1, AI994545.1, F14085"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochtemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project
lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project
lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project
lemcke@mips.blochem.mpg.cev.cect
lemcke@mips.plohn.lnnes Centre.cect
lemckerenter Michael.bevan@bbsrc.ac.uk
Lerck,R., De Keyser,A., Neyt,P., Rouze,P., Van Den Daele,H., Villaroel,R., Gielen,J., Van Montagu,M., Hoheisel,J., Mewes,H. Lemcke,K. and Mayer,K.F.X.
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11225. .11425,11998. .12039))
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                                                                                                                                                                                                                         Bevan,M., Volckaert,G., Grymonprez,B., Voet,M., Rok
Hoheisel,J., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
Unpublished
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/db_xref="G1:368171"
/db_xref="GOA:082633"
/db_xref="SPTREMBL:082633"
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1 (Dasses I to 94482)
Bevan,M., Terryn,N., Ardiles,W., Buysshaert,C., Dasseville,R., De
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                                                                                                          CTTTCATTGAGTCTTGCATCAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCA
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	/1//1//1//1//	intron 13748 .14080 /gene="Ar4932910" /number=5 exon /gene="Ar4932910" /number=6 intron /gene="Ar4932910" /gene="Ar4932910" /number=6 exon /4381 .14491 /meha="Ar4932910"	intron (492. 14595 /gene="AT4932910" /number= AT4932910" /gene="AT4932910" /number= 87 intron (4634. 14717 /gene="AT4932910" /number= AT4932910" /number= AT4932910" /number= AT4932910" /number= AT4932910" /number= AT4932910" /number= AT4932910"	Query Match 58.9%; Score 1110.6; DB 8; Length 94482; Best Local Similarity 92.7%; Pred. No. 1e-241; Indels 92; Gaps 1; QY 283 ATAAAGTTCATAGAAACCCAATGGAACACAACAACAACAACAACAACAACAACAACAACAAC	47774 523 47714 47654 643
			intron complement(11426, .11997) /gene="Artg32900" /number=4 complement(11998, .12039) /gene="Artg32900" /number=5 12433, .17137 /gene="Artg32900" /gene="Artg32900" /gene="Artg32900" /gene="Artg32900" /gene="Artg32900" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /gene="Artg32910" /codon_gene="Artg32910"	/product = 'product = 'profein" /protein id="CAA21200" /db_xref="dI:3688172" /db_xref="dI:3688178" /db_xref="d	exon 12433 12800 gene="AT4932910" number=1 12801

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KRANYOPOKGSANORNGSDHGNUSYYEPDYPKGLIISFTLKRSAEBGTTEOKESBEPT
DKYMESESTFYRADTPDADKRNTGEVQAEGAEDEDDEKEEKGALATHKDNKDVLLREDL
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VIVKMSLVYIALCOAKLKRSIGLSYBAKIGLTRVAVEGEFFFCLVLQIIIXLVYAGE
                                                                                                                                                                                                                                                                                                                                                                                                           Terryn, N., Ardiles, W., Buysshaert, C., Dasseville, R., De Clerck, R., De Keyser, A., Neyt, P., Rouze, P., Van Den Daele, H., Villaroel, R., Gielen, J., Van Montagu, M., Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-MRR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de_project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevar@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV73 at the 5' end and an overlap with ATCHRIV73 at the 5' end and an overlap with ATCHRIV73 at the 5' end and an overlap with ATCHRIV77 at the 5' end and an overlap with ATCHRIV77 at the 5' end and an overlap with ATCHRIV77 at the 5' end and an overlap with ATCHRIV77 at the 5' end and an overlap with ATCHRIV77 at the 5' end and an overlap with ATCHRIVATOR ATCHRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 (bases 147462 to 198669)
Peters,S.A., van Staveren,M., Dirkse,W., Stiekema,W., Mewes,H.W.,
Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (bases 157520 to 158319; 162782 to 163400; 178485 to 179218; 182013 to 182758)
Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
                                                                                                                                                  2 (Dases 38710 to 90803)
Lennard,N., Quail,M., Harris,B., Rajandream,M.A., Barrell,B.G.
Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
Unpublished
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                    Borkova, D., Ansorge, W., Mewes, H.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 38818)
Benes, V., Rechmann, S., Bor
Lemcke, K. and Mayer, K.F.X.
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                                                     ATGTCTACATTCGGTGAAGAATTTTCCCGTTTCTAATTTTCGAATAAAGAAACAATGAG
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KEYWORDS
SOURCE
ORGANISM
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9122. .9224 /gene="AT4g32720"

intron

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,

9071. .9121 /gene="AT4g32720"

'number=

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Query Match Best Local Similarity	RESULT 10	RESU
DVV AA: ORIGIN	1451 CTGTTTCGGTCTACGAATTCGATGTTCCAAACTTCCTTACCTTACC 1501 	o o
III HAY	137450 AGCAGCTGAAACGAAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAAT 137391	qa
₹₩.	1391 AGCAGCTGAAACGAAGGAACCATCAGAGACCTCAACGAGGTTTGCCTGAGAAAT 1450	ζ
ia (₹)	137510 TGGAGAGAGAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTTC 137451	qq
A88	1331 IGGAGAGGCAAAGACTCAAGAAACCTCTATGTTCCACCAGGATTGCCTTCTTC 1390	ò
กับ 🍾	137570 TCTTATACAAGAAACCTGAGAGAGAGAATCTGCAAGAAGATATCTCTATGGGATCTGTAT 137511	QQ
SDS CDS 6	1271 TCTTATACAAGAACCTGAGAGAGAATCTGCAAGAAGATAATCTCTATGGGATCTGTAT 1330	λŏ
gene 93	137630 ATGCTGCAACCGAGTTAGATCCACAGTTACACACCGGTTTGCCCTCCAAACCGTTTCCT 137571	qq
misc_reature /v	1211 ATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAAACCGTTTCCT 1270	ò
	137690 AGGIGGATGATGGTCATIGCGTAGAGATGAGATTCATACGGTTATATCAGCGTTCC 137631	Dp
misc_signal 78.	1152 -GGTGGATGATGGATATAGTCATTGCGTAGATGAGATTCATACGGTTATATCAGCGTTCC 1210	ò
misc_signal co	137750 ATAAGTTAAAAAATGGTTTGATATATATGAGTTTTATGAGTTTGATTATT	qq
1	1152 1151	ò
misc_feature 20	137810 AAAACCCATCTTTGGATCTTCTTCAAATGGTATGTAATATTCATTC	g
misc_signal 47/	1123 AAAACCCATCTCTTGGATCTTCTTCAAAT	à
ū/	137870 TCTAATAACTCGGAGGGGTTTCGGATCTACATTTCAAAGGAGAGCATTAGAAGCAAAG 137811	d
misc_feature 1.	1063 TCTAATAACTCGGAGGCGGGTTTTGGATCTACATTTCAAAGGAGGGTTTAGAAGGAGAAG 1122	ò
0 0	137930 GCTGCTAGTTCAGCCTTTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGAT 137871	QQ
> 10 (1003 GCTGCTAGTTCAGCCTTTTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGAT 1062	δλ
O É ,	137990 ATACTATCTCATTTGGCGGCATACTCGGTTGATTTTTCATCTCGAGGAACCGAGTCAGGA 137931	QC
rearones Lo source 1.	943 ATACTATCTCATTTCGCCGCATACTCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGA 1002	ò
	138050 GTTACTCAAGGTTTCTCTCAACTTATTTGGCTCAAAATACCTTCACTCGTTCAAGAA 137991	QC
JOURNAL Submitted (883 GTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTTCACTTCAAGAA 942	ò
AUTHORS Oosterling,	138110 GCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAGAAGACATTTCTAATAACGTT 138051	QQ
) W W	823 GCTACAAGATTAGCCTCAGAGCTTCTTGCAGCAGAAGACATTTCTAATAACGTT 882	ò
Arabidopsis JOURNAL Nucleic Aci	CITICATTGAGTCTTGCATCAGATGTTTCTGATGATGATGCTCGGAGATAAGTCTTTGTGCA	ପ୍ର
TITLE Analysis of	いって、その他の世界が出くさればないのの思いでは、そのはより他の世界の世界ではないない。	č
	138230 AIGICTACATICGGIGAAGATITCCCGTITCTAATITCGAATAAAGAAACAAIGAG 138171	Db
REFERENCE 1 (bases 1	703 ATGICTACATTCGGTGAAGAAGATTTCCCGTTTCTAATTTCGAATAAAAGAAACAATGAG 762	δ
Spermatophy	138290 TITGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATG 138231	qq
SOURCE Arabidopsis ORGANISM Arabidopsis	643 TITGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATG 702	ò

PLN 10-SEP-1997

linear

DNA

ATZ83320 A.thaliana partial ATH1 gene. 283320 283320.1 GI:1865680 ATH1 gene; MAR.

ATZ83320 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Varia Magnollophyta, eddicotyledons, core eudicots, 1rosida II, Brassicales, Brassicaceae, Arabidopsis.
1 to 10072)
1.C.M., Oosterling, R.W., Keultjes, G.M., Weisbeek, P.J., van and Smeekens, S.C.
2f the chromatin domain organisation around the in gene reveals an MAR-specific sequence element in is thaliana.
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note="ATH1 MAR-2 MAR-specific sequence signature"
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note="ATH1 MAR-3 MAR-specific sequence signature"
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note="ATH1 locus MAR-1"
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mol_type="genomic DNA"
variety="Columbia-0"
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SM Iycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

El (Asses It ol 182)

Ron, N., Parnis, A. and Lifschitz, E.

Direct Submission

Location/Qualifiers

| Submitted (03-MAY-2001) Biology, Technion, Haifa, Israel
| Location/Qualifiers

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bell-like homeodomain protein 4 (BL4) mRNA,
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KRCDHQLMRPQRGIRESRSVSTLRAMMFQNFLHPYPKDAEKQLLAVKSGLTRSGVSNWF
INARVRLWKPMIEEMYAEMNRRKIRAGNEEDHRRNHKIIESHLFTMK"
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                                                                                                                                                                                                                                                                                                               Score 255, DB 8; Length 1182;
Pred. No. 2.8e-47;
), Mismatches 290; Indels 3
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CCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGT
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1. .2735
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148. .2214
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Chen,H., Rosin,F.M. and Hannapel,D.J.
XNOX protein of potato interacts with several members of the TALE
family of transcription factors
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SVRKAIKEQNSKKELTKDSRESDVDSKNISSDTPANGGSNPHESKNNOSELSPTEKQE
                                                                                             AF406703 2065 bp mRNA linear PLN 14-JUL-2003
Solanum tuberosum BEL1-related homeotic protein 30 (Bel30) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQNKLAKLLSMLDEIDRRYRQYYHQMQIVVSSFDVVAGEGAAKPYTALALQTISRHFR
CLBDLTCDR CASREGLGOASENSKAIGISRLRYDHHIRQQRALQQLGMMQDHAW
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KPWYBEMYKEEAGDAKIDSNSSSDVAPRLATKDSKVEERGELHQNAASEFEQYNSGQI
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GSFGSGNVLPNGVSLTLGLQQGEGSNLPMSIETHVSYVPLRADDMYSTAPTTMVPETA
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1 (bases 1 to 2065)
Chen,H., Rosin,F.M., Prat,S. and Hannapel,D.J.
Interacting transcription factors from the three-amino acid loop extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003)
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Chen, H., Rosin, F.M. and Hannapel, D.J.
Direct (Submission
Submitted (07-ANG-2001) Department of Horticulture, Iowa State
University, 257 Horticulture Hall, Ames, IA 50011-1100, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Desiree"
/db_xref="taxon:4113"
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Solanum tuberosum
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                                                                                                              DEFINITION
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                                                    RESULT 12
AF406703
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WRRPVEBMYLEBVXNQQQNSTNYSGDNKNKETNISAPNBEEKHPITLSSLLQDGTYTTQ
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GLPPSENLAMPVSQONYLSNDLGSRSEMGSHYNRMGYENIDFQSGNKRFFPTQLLPDFV
TGNLGT" 2735 bp mRNA linear PLN 14-JUL-2003 Solamum tuberosum BEL1-related homeotic protein 5 (Bel5) mRNA, AF406697 2 (bases 1 to 2735)
Chen,H., Rosin,F.M. and Hannapel,D.J.
A KNOX protein of potato interacts with several members of the TALE family of transcription factors
Unpublished 1614 1347 CAGGTATCAAATTGGTTCATAAATGCACGGGTGCGTCTTTGGAAACCCATGGTTGAGGAA 1406 Solanum tuberosum (potaco)
Solanum tuberosum (potaco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterida; lamidas; Solanales; Solanaceae; Solanum.
I (bases 1 to 2735)
Chen, H., Rosin, F. M., Prat, S. and Hannapel, D.J.
Interacting transcription factors from the three-amino acid loop extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003) 1287 CCCTACCCGAAAGATTCTGACAAAATTATGCTAGCAAGGCCAAACTGGCTTAACGAGAAGT CAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAG 3 (bases 1 to 2735) Chen.H., Rosin.F.M. and Hannapel, D.J. Direct Submission Submitted (07-AUG-2001) Department of Horticulture, Iowa State University, 257 Horticulture Hall, Ames, IA 50011-1100, USA

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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Oohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., International Science Genome Sequencing & Analysis Group; Otomo, Y., Murakami, K., Idaa, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Rusawaki, T., Kodama, T., Masuka, Y., Yokomizo, S., Niikura, J., Rusumegi, T., Oka, M., Kaya, R., Yoshimura, A., Mikura, J., Rusumegi, T., Oka, M., Kaya, K., Voshimura, A., Mikura, J., Rawai, J., Carninci, P., Adachi, W., Masubara, K., Ishii, Y., Itch, M., Kagawai, T., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshimo, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimira, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Fujimira, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashizaki, Y., Hayashizaki, W., Hayashizaki, W., Hayashizaki, W., Hayashizaki, W., Hayashizaki, W., Hayashizaki, W., Ishizika, M., Itoh, M., Kagawa, T., Hotta, I., Iida, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Karch, H., Kawagashira, N., Kawa, J., Koma, S., Komno, B., Konda, M., Kodama, T., Kojima, Y., Kondo, S., Konno, B., Konda, M., Koya, S., Kurihara, C., Kurosashi, T., Milazina, K., Murata, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Makamira, M., Maiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Nikura, J., Nishi, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ryu, R., Saltoh, H., Sakai, C., Sakai, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) cDNA clone:J013124105, full insert sequence.
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FIL CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae;
                                            CAGCATTGCCTTCTTCAGCAGCTGAAACGAAGCAACCATCAGATTTGGAGACCTCAACGA
                                                                                                                                                                                                                                                                                                                                                    CCTTACCCGAAAGATTCGGAGAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGT
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/ GOGOD STRIKE:
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FHGNNGVSLTLGLPPSENLAMPVSQQNYLSNELGSRPEIGSHYNRMGYENIDFQSGNK
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                                                                                                                                                                                                                                                                                                                                                    1339 GGITTTACCTGAAAGAGCTGTCTCTTCGTGCTTTGGCTTTTTCGAGCATTTTCTTCAT 1398
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Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Solanales, Solanaceae, Solanum, Lycopersicon.
I (bases I to 2636)
Ron, N., Parnis, A. and Lifschitz, E.
Direct Submission
                                                                                                                             1375 CAGCATTGCCTTCTTCAGCAGCTGAAACGAAACCAACCATCAGATTTGGAGACCTCAACGA
                                                                                                                                                                                                      1279 CAACAACGCGCGCTGCAACAGATAGGAATGATGCAACCAAATGCTTGGAGACCCCAAAGA
                                                                                                                                                                                                                                                                                    1435 GGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                          1495 CCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGT
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                                                    Indels
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1.4e-18;
            66.3%; Pred. No. 1.4e
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AF375966
AF375966.1 GI:31323446
                                                    Conservative
                Local Similarity
                Best Local Simi
Matches 185;
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RESULT 14 AF375966 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

source

CDS

ORIGIN

REFERENCE AUTHORS TITLE JOURNAL FEATURES

Search completed: September 2, 2004, 08:22:51 Job time : 7423 secs

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Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fuls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fuls Genome Sequencing & Ishibik,J., Kawamata,M., Kobayashi,M., Kodama,T., Kuroashi,T., Kusumagaj,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimra,A., Marsubara,R. and Murakami,K. Genome Exploration Research Group in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carnind,P., Fukuda,S., Hanaco,K., Hara,A., Hashizume,W., Hayashida,K., Hayastu,M., Hiramcto,K., Hiracka,T., Hori,F., Iida,J., Imamira,K., Haracta,M., Kanagawa,J., Kanagawa,S., Katoh,H., Kawai,J., Kouda,M., Kishikawa-Hirozana,T., Kojima,Y., Kondo,S., Konno,H., Kowa,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Ota,Y., Saltoh,H., Sakai,C., Sakai,K., Sakazume,M., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sakathashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., Tagami,M., Tagami,Y., Toyaru,A., Toya,T., Waki,K., Yasunishi,A., Tagami,Y., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., Tagami,Y., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., Toya,T., Yasunishi,Y., Toya,T., Toya,T., Waki,K., Yasunishi,A., Toya,T., Toya,T., Toya,T., Waki,K., Yasunishi,A., Toya,T., Toya,T., Toya,T., Yasunishi,A., Yasunishi,A., Toya,T., Toya,T., Toya,T., Toya,T., Waki,K., Yasunishi,A., Toya,T., Yasunishi,A., Toya,T., Yasunishi,A., Toya,T., Toya,T., Toya,T., Waki,K., Yasunishi,A., Shinagawa,Y., Toya,T., Toya,T., Yasunishi,R., Yasunishi,A., Toya,T., Yasunishi,R., Toya,T., Toya,T., Toya,T., Yasunishi,R., Yasunishi,A., Toya,T., Toya
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Rishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MS-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Suguyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Towaru, Y., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
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/mol type="mRNA"
/culTivar="Nipponare"
/culTivar="Laxon:3947"
/clon="J013124105"
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6.7%; Score 126.4; DB 8; Length 2570; 68.4%; Pred. No. 4.5e-18; ive 0; Mismatches 81; Indels 0;

Conservative

Matches 175;

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Query Match Best Local Similarity

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1375 CAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGCAACCATCAGATTTGGAGACCTCAACGA

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1602 CCGTATCCAAAAGATTCAGAAAAGCTGATGCTAGCGAGACAAACTGGCTTAACAAGAAGT

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Aag321086 Arabidops
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Aab32893 Pinus rad
Aab32893 Pinus rad

Sequence:

Run on:

Searched:

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us-09-423-575-1.rag
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Grass; plant; herbicide resistance; grass flowering inhibitor; baseball; cricket; football; golf; rugby; soccer; tennis; lawn; park; athletic field; animal feedstuff; AtHl protein.
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27-NOV-2000; 2000US-0253274P.
27-NOV-2000; 2000US-0253327P.
22-JUN-2001; 2001US-0300220P.
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N-PSDB; ABK11039.
 WO200214524-A2.
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ID AAU7
  Aau76514 Arabidops
Aau76885 Arabidops
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              OM nucleic - protein search, using frame_plus_n2p model
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                                                                                               The invention relates to a grass plant, which has been genetically modified to substantially inhibit generative propagation and carry herbicide resistance. The grass is useful for growth and/or propagation of grasses. The grass is used to play at least one sport (e.g. baseball, cricket, football, golf, rugby, soccer or tennis), or used at least in portion of an athletic field, lawn or park. The grass is fed to animal (e.g. cattle, goat, horse or sheep) or used as an animal feedstuff. The present sequence represents the amino acid sequence of Arabidopsis Athl protein, which was used to inhibit flowering in grasses
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New genetically modified grasses that express inhibited generative propagation, or herbicide resistance, useful for forage (e.g. cattle feedstuff) or amenity purposes (e.g. for use in an athletic field, lawn
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             281 LeuGinMetValAspAspArgTyrSerHisCysValAspGluIleHisThrValIleSer
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                                                                                                   TTCGGATCTACATTTCAAAGGAGGAGTATAGAAGCAAAGAAAACCCCATCTTGGATCTT
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Arabidopsis thaliana. WO200214486-A2

21-FEB-2002

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modified to substantially inhibit generative propagation. The genetically modified to substantially inhibit generative propagation. The genetic modification may result in a heritable change in one or more plant characteristics such as inhibition of flowering (or substantial delay trat amounts to inhibition), absence of inflorescence, increased correct that amounts to inhibition), absence of inflorescence, increased correction of tillers, delayed heading and inhibition of the developmental switch from vegetative to generative growth. A method of making a grass involves transforming the grass with a nucleic acid which applying a phytohormone to at least partially relieve or reverse a change in plant characteristic resulting from genetic modification. The correction genetically modified grass is useful for growing and/or propagating grass in athletic fields (for sports such as baseball cricket football, golf, rugby, scocer and tennis), lawns, parks and other types of landscaping. The grass is also useful as an animal feedstuff for cattle, goats, horses and sheep, due to its increased vegetative growth, improved digestibility and/or nutritional value as animal feedstuff. This sequence represents the Arshidopsis thaliana homeobox gene Athl encoded protein. Athl is
                                                                                                                                                                                                                                                                                                                                                                    New genetically modified grass useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), or as animal feedstuff for cattle, goat, horse and sheep.
                                                                                                                                                                                                                                             Van Der Valk P, Van Dun CMP, Smeekens SCM, Proveniers MCG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed by various transgenic grasses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 6; 45pp; English.
                                                                    18-AUG-2000; 2000US-0226422P.
27-NOV-2000; 2000US-0253274P.
27-NOV-2000; 2000US-02533277
22-UUN-2001; 2001US-0300220P.
                       16-AUG-2001; 2001WO-EP009570.
                                                                                                                                                                                              (ADVA-) ADVANTA SEEDS BV.
                                                                                                                                                                                                                                                                                             WPI; 2002-257603/30.
N-PSDB; ABK10687.
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XX SQ Sequence 473 AA;			
Alignment Scores:			
Pred. No.:	5.45e-250	Length:	473
Score:	2484.00	Matches:	473
Percent Similarity:	100.00\$	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.64%	Indels:	0
DB:	2	Gaps:	0
(577-1) 300251144 × (3001-1) 1-353-557-00-511	300351144 \$ (3)	(5-7-5)	

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	Scores: Similaritati	es: irity: iilarity:	5.45e-250 2484.00 100.00\$ 100.00\$ 75.64\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	4 4 7 3 3 4 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
US-09-423	1-575-	.1 (1-1886	US-09-423-575-1 (1-1886) x AAU76885 (1-473)	473)		
δλ	304		AACAACAACAAC	ACTITIAGITICICIE	ATGGACAACAACAACAACAACACTTTTAGTTCTCTGGATAATGTCATGACTAACCAA	363
Db	П	MetAspAsn				20
٥'n	364		CTCATGGATTTTATA	CCTTCAAGAGAAGAT	AATCCTCTTCTCATGGATTTTATACCTTCAAGAGAAGATTCAACTTCATCAACAATG	423
Db	21	AsnProLeu				40
٥'n	424	CTTCCATGG	AATACCATCAGATCA	GATCCTCTACAAATG	CTTCCATGGAATACCATCAGATCCTACAAATGGGTGGCTTTGATATTTTCAAT	483
Db	41	LeuProTrp	AsnThrileArgSer		LeuProTrpAsnThr1leArgSerAspProLeuGlnMetGlyGlyPheAspIlePheAsn	9
٥;٨	484	TCTATGCTG	ACTAACAAATACTT	ATCATCTTCTCCACGG	TCTATGCTGACTAACAATACTTATCATCTTCTCCCACGGTCTATCGATGTTCAAGATAAC	543
Db	61	SerMetLeu	ThrAsnLysTyrLev			80
λŏ	544		GAGTTCATGGCTCCT	CCTCCTCATCCTCCT	CGCAATGTTGAGTTCATGGCTCCTCCTCCTCCTCCTCCACTTCATCCTTTGGATCAT	603
Db	81		GluPheMetAlaPro		ArgAsnValGluPheMetAlaProProProHisProProProLeuHisProLeuAspHis	100

	604	99
	101	
	664	72
	121	14
Sy B	724	724 GATTICCCGTITCIAATITCGAATAAAAGAAACAATGAGCTITCATIGAGICTIGCAICA 783 14
	784	84
	161	18
٥y	844	CAAGCTTCTTGCAGCAGCAATTTCTAATAACGTTGTTACTAAGGTTTCTCTCAA 903
qq	181	N
	904	CITAIAITIGGCICAAAATACCITCACICIGTICAAGAAATACIATCICATITCGCCGCA 963
	201	
ολ	964	TACTOGCTOGATTATTCATCTCGAGGACCGAGTCAGGAGCTGCTAGTTCAGCCTTTACT 1023
	221	
٥٧	1024	-
	241	
٥٧	1084	11
	261	0
	1144	12
	281	LeuglnMetValAspAspArgTyrSerHisCysValAspGlulleHisThrValIleSer 300
٥٧	1204	12
	301	32
۵,	•	GTTTCCTTCTTATACAAGAACCTGAGAGAGAATCTGCAAGAAATCTCTATGGGA 1323
Д	321	ValserPheLeuTyrLysAsnLeuArgGluArgIleCysLysLysIleIleSerMetGly 340
٥٨	1324	TCIGIATIGGAGAGAGAGAAGACAAGACTCAAGAAACCTCIATGTTCCACCAGCATIGC 1383
Db	٧.	0
٥y	1384	CITCHICAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTCCT 1443
, QO	361	LeuleuGlnGlnLeulysArgLysAsnHisGlnIleTrpArgProGlnArgGlyLeuPro 380
٥٧	1444	GAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCCTTC
DÞ	381	GlulysSerValSerValleuArgAsnTrpMetPheGlnAsnPheLeuHisProTyrPro 400
٥٧	1504	AAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCA 1563
qu	401	
٥٧	1564	AACTGGTTTATAAATGCGCGGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCG 1623
Db		
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Db	441	GluMetAsnLysArgLysLeuAsnAsnSerHislleGlnProAsnGlyProThrLeuArg 460

Qy 514 TCTCCAGGTCTATGATGTTCAAGATAACCGCAATGTTGAGTTCATGGCTCCTCCTCTTCT	Qy 574 CATCCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATTCCTCAAACAAC	Db 111 ValGlnTyrSerLeuTyrGlySerHisGlnValAspProThrHisGln	Qy 634 ATGTGGGGTTTTGAAGCAAATAGTGAGTTTGAGGCATTTTGAGGTGTAGTTGGTCCAAGT	Db 127 GlnAlaAlaCysGluThrProArgAlaGlnGlyLeuSerLeuThrLeuSerSerGln	Qy 694 GAACCAATGATGTCTACATTCGGTGAAGAATTTCCCGTTTCTAATTTCGAATAAAAGA	Db 147 GlnGlnGlnGlnGlnHisHisHisGlnFroIleHisValGlyPheGlySer	QY 754 AACAATGAGCTTTCATTGAGTCTTGCATGAATGTTTCTGATGAATGCTCGGAGATAAGT	Db 167	Qy 814 CTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAGACATTTCT	Db 177GlySerThr		180		199	Qy 994 GAGTCAGGAGCTGCTACTTCAGCCTTTTACTTTGAGAATATAA	213	г	Db 233 ProvalGlyGluSerSerAlaGlyAlaGlyGluGlySerGlyGlyGlyA.	H	253	Н	6/3	Qy 1186 ATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACGGTTATACAC :::	Db 293 MetGlnMetValileSerSerPheGluGlnAlaAlaGlyIleGlySerAlaL	Qy 1243 ACCCGGTTTGCCCTCCAAACCGTTTCTTATACAAGAACCTGAGAGAGA	313	1303 AAGAAGATAATCTCTA	333GlyGlnIleLysAlaAlaAsnLy	9y 1363 TCTATG	34/ ServalSerGlyvalGlyArgFneGluGlySe		,	OV 1423 AGACCTCAACGAGGTTTGCCTGAAATCTGTTCGGTTCTACGGAATTTGGATTCTGTTCTACGGAATTGGATTGTTCCAA
1684 ATGCCAAAATCTGTTATGATGAGCAAGCAATGCATAAA 1722 	, and the second se	ısu ADB23150 standard; protein; 680 AA.	ADB23150;	20-NOV-2003 (first entry)	Environmental stress-responsive promoter-related protein, SEQ ID 154.	Plant; environmental stress; promoter.	Arabidopsis thaliana.	WO2003044190-A1.	30-MAY-2003.	5-NOV-2002; 2002WO-JP011955.	9-NOV-2001; 2001JF-00353038. 9-JAN-2002; 2002JF-00020329.	(RIKE) RIKEN KK,	Shinozaki K, Seki M, Fujita M;	WPI; 2003-468771/44.	N-PSDB; ADB23149.	Environmental stress-responsive promoters, useful in constructing and breeding stress-resistant plants for applications in agriculture.	Claim 9; Page 476-480; 520pp; Japanese.	e present invention relates to novel environmental stress-responsive	promoters (ADB23163-ADB23252) from Arabidopsis thaliana. The promoters are useful in constructing and breeding stress-resistant plants for	applications in agriculture and norticulture. The present sequence was used to illustrate the invention.	Sequence 680 AA;	Scores:	1.12e-39 Length: 472.00 Matches:	2.01% Conservative: Mismatches:	14.37% Indels:		283 ATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAACAACATTTTAGTTCTCTG 342	32 ValdinTyrThrGlnGlnAspAsnAspSerAsnAsnAsnAsnAsnSerAsnSerAsn	343 GATAATGTCATGACTAACCAAAATCCTCTTCTCATGGATTTTATACCTTCA 393	:::	394 AGAGAAGATICAACTICATICICAAGAAAIGCTICCAIGGAATACCAICAGAICAG	72 HisAlaPro-GinProAsnAlaSerGinGlnPheValGiyileProLeu 87	

	3 TTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGGGGTTAGGGTATGGAAGCCG 1602 		3 CCCAACGACCAACTCTTCGAATG 1686	7 GlulysThrProLeuAspGlnSerAsnGluAspSerAlaSerLysSerThrSerAsnGln 486	7 CCAAAATCTGTTATGATGAGCCAAGCAATGCATAAATAAGACAACAAT 1734 		***	2004 (first entry)	ield-related protein from clone G1589.	cription factor; transgenic plant; growth rate; senescence; germination rate; plant vigor; seedling vigor.	osis thaliana.	13227-A2.	-2003.	2002; 2002WO-US025805.	2001; 2001US-0310847P. 2001; 2001US-0336049P. 2001; 2001US-033692P. 2002; 2002US-00171468.	MENDEL BIOTECHNOLOGY INC.	fe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE; ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G; E;	03-248221/24. ADD30303.	'plant transcription factor polynucleotides and polypeptides, useful producing transgenic plants with commercially valuable properties, ih as an alteration in a plant growth characteristic, e.g. growth rate apomixis.	ure; SEQ ID NO 333; 454pp; English.	The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transpenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an altered desirable traits as compared to a reference plant, such as an altered desirable traits as compared to a reference plant, such as an altered desirable traits of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgent plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the proteins of the invention.
::: HisPheLeu	TTGACAAGA LeuThrArg	ATGATAGAA ::: MetValGlu	CCCAACGG	GluLysThr	CCAAAATCI	standard;		4,	φ'	facion	thali		003.	. 5	001; 20 001; 20 001; 20 002; 20	MENDEL BIC	ם	3-248221/: ADD30303.	t transcr. cing trans an altera xis.	SEQ	ntion rel s and the elated CD ption fac g transge of transge an altera ion rate enescence peptides ic plant
407	1543 42 ⁷	1603	1663	467	1687	JLT 4 10304 ADD30304	ADD30304;	15-JAN-200	Plant yie	transcription seed germinat	Arabidopsis	WO2003013227	20-FEB-20	09-AUG-20	09-AUG-20 19-NOV-20 11-DEC-20 14-JUN-20	(MEND-)	Ratcliffe O, Pilgrim ML, Broun PE;	WPI; 2003-2482 N-PSDB; ADD303	New plant to in producing such as an or apomixis	Disclosure;	The invention sequences and factor related transcription producing transcription as an alternation reliance senesce and polypeptic transgenic plating seguences.
Db	Sy qq	S S	ò	QQ	8 8	RESULT ADD303 ID A	X Z S	X E X	S E S	(BB)	SS S	X E	(교)	4 분 3	4 K K K K K K	X &	X I I I I	4 E E E	4 F F F F F	Z S	¥88888888888888

	Alignment Pred. No.: Score: Percent S: Best Local Query Matc	Sco : :mil : Si	res: arity: milarity:	1.12e-39 472.00 42.01% 28.25% 14.37%		Length: Matches: Conservative: Mismatches: Indels:	847 8346 846 846 846 846 846 846 846 846 846 8	3 6 3 5 5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7		-		
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	<u>ک</u> د	283	ATAAAGTTT :::::::: ValGlnTyr	CATAGAAA ::: ThrGlnGl	CCCAATGGACAA :: nAspAsnAspSe	CAACAACA - rAsnAsnA	CAA TAB	ACA - : snS	CTTTTAGTTC :: :: erAsnAsnSe	rcrcrg erAsn	342	
	ζō	343	GAT	AATGTC	CATGACTA	AACCAAAATCCTCTTCTCATGGATT	TCT	ZATGG?	TTTTATAC	U-	393	
	QQ	22	::: AsnAsnAsn	; nAsnAsnThrAsnThrAsnThrAsnAsnA	 AsnThr?	 snAsnS	erSe	rPheVa	::: erPheValPheLeuAspS	AspSer	71	
	70	394	AGAGAAGATT	TCAACTTC	ATTCTCA!	CAACTICATICICAACAATGCTICCATGGAATAC	GAA7	FACCAT	CATCAGATCAGATCCT	BATCCT	453	
	Db	72	HisAlaPro		nAlaSer	rGlnGlnPheValG	Glylle	LeProL	en		87	
	δλ	454	CTACAAATG	ACAAATGGGTGGCTTTGATATTTT	GATATT	ITCAATTCTATGCTGACTAACAAA	GACT	raaca?	TACT	CATCT	513	•
	Op Op	89							SerGlyH	/His	90	
	ογ	514	TCTCCACGG	Ē-	GTTCAAC	τj	rrga(3TTCA:	CATGGCTCCT	CCTCCT	573	
	Dβ	91	GluAlaAla	Serile	ThrAlaAlaA	spanileserv	alLe	euHisGl	yTyrèrob	ProArg	110	_
	٥٨	574	CATCCTCCT	CCACTIC	CCTTTGGAT	GATCATTTAAGACA	CTA	CTATGATG	GATTCCTCAAA	AACAAC	633	
	qq	111	ValGlnTyr	SerLeuTyrGly			- 8G11	nValAsp	pProThrH:	HisGln	126	
	ò	634	Argregest	ATGTGGGGTTTTGAAGCAAATAGTGAGTTT	AAATAGTO	GAGTTTCAGGCATTTT 		CAGGTGT.	AGTTGGTC	CCAAGT	693	
	DB DB	127	GlnAlaAla	CysGluThr	rProArgAl	aGlnGlnGl	yLeuse	rLeuT	user	SerGln	146	
	ò	694	GAACCAAT	GATGTCTACA	ATTCGGT	AGAAGATTTC	CCGTTT	TCTAA	CTAATTTCGAATAAAG	aaaaga	753	
	Db	147	GlnGlnGl	nGlnGlnGl	nHisHis	sGlnGlnHisGlnFr	roll	eHisVa	lGlyPhe	Glyser	166	
	λ̈́	754		AACAATGAGCTTTCATTGAGTCT	SAGICIT	GATGTTT	CTGAT	TGAATG	CTCGGAGAT	ATAAGT	813	
	Db	167	::: GlyHisGl	:: yGluAspIle	eArgVal	GlySer		1	1	1	176	
	δλ	814	CITIGI	GCTACAAG	ATTAGCC	GCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAAGACAT	TTG	CAGCA(CAAAGAC	ATTTCT	873	
	QQ	177	1				i		Gly	Ë	179	_
	ò	874	AATA	4 —	CTCAAGGTTTC:	rcaacttatat : :::	TTGG	TGGCTCAAAATA	CCTT	51.	93	
	Db	180	Gly	valThrAsnGlyIl	idly11e	eAlaAsnLeuVal	Se	rserly	sTyrLeu		198	_
	<i>ک</i>	934	GTT	AATACTATC	rCATTTC	CAAGAAATACTATCTCATTTCGCCGCATACTCGCTCGATTATT	rcga:		CATCTCGAGGAAC	3GAACC	993	
	Dþ	199	AlaGlnGl	ureureuAsı	oGluVal	laAspS	erAs	- a	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		212	
	8.	994	GAGTCAGGAG	AGCTGCTAGTTCAGCCTTTACTT	FTCAGCC	0	rtga(SAATAS	-	ACTGAGTTT	105	o
	Ор	213	AspMetA	snAlaLysSe	erGlnLeu	erLy	/sGly	Se	sGlyAsnA:	6	232	
	₺.	1051	CLL	rrctaa .!!!	raactege.	GAGGCGGGTTTCGGA'	BATCT		1		109	2
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	QQ	253	AlaGlyLysAr	gProVa]G]nren	GluLeuGlyThrAlaGluArgGlnGluIleGl	rgGl	ngluI	eGlnMet	nMetLysLys	272	۸.
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XX SQ Sequence 680 AA;

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  .186 ATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTA---GATCCACAGTTACAC 1242
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1126 ACCCATCTTGGATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAG 1185
                                                                            1303 AAGAAGATAATCTCTATGGGATCTGTATTGGAGAGGGCAAAGACAAGACTCAAGAAAC 1362
                                                                                                                                                        -----TICCACCAGCAITGCCIT 1386
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                                                 TTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCG 1602
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            273 AlalysleuSerAsnMetLeuHisGluValGluGlnArgTyrArgGlnTyrHisGlnGln 292
                                                                                     347 ServalSerGlyvalGlyArgPheGluGlySerArgLeuLySPhevalAspHisHisLeu 366
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367 ArgGinGinArgAlaLeuGinGinLeuGlyMetIleGinHisProSerAsnAsnAlaTrp 386
                                                                                                                                                                                                                                                                                           426
                                                                                                                                                                                                                                                                                                                              LeuThrArgSerGlnValSerAsnTrpPhelleAsnAlaArgValArgLeuTrpLysPro 446
                                                                                                                                    -------dlyGlnIleLysAlaAsnLysSerLeuGlyGluGluAsp 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                             -----CTGAAACGAAAGAACCATCAGATTTGG
                                                                                                                                                                                                                                                                                    CCAAAATCTGTTATGATGAGCCAAGCAATGCATAAATAAGACAACAAT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 GluLysSerProMetAlaAspThrAsnTyrHisMetAsnProAsnHis 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 14933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG14898 standard; protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                          1663 CCCAACGGACCA------
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99US-0123180P,
99US-0123548P.
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                                                                                                                                                                                            1387 CTTCAGCAG-----
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                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 14932.
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                                 ------AsnGlyLysSerLeuSerValHisGlnHisHisSerAspGlnIleLeuPr 129
                                                                                     129 oSerSerVal-----TyrAsnAs 135
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          747 TAAAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTTTCTGATGATGCTCGGA 806
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294 pAlaileLysGluGlnIleGlnValileArgGlyLysLeuGlyGluArgGluThrSerAs
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14-JUN-1999;
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17-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
21-JUN-1999;
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1674 AACTCTTCGAATGCCAAAATCTGTTATGATGAGCCAAGCAATGCATAAA----- 1722
                                            ----TAAGACAACAATTGTGTTTACCAACTTTGTGATAATTA 1760
                              447
414 sGluGluPheGlyGluSerAlaGluLeuLeuSerAsnSer------AsnGlnAs 430
                                                       Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                        1761 GGCAATTGCTACTCTATGATTGCCCAAAACCTAAAACCATGTACGACT 1807
                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 14931.
                                                                                                                         AAG14896 standard; protein; 533 AA
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99US-0123180P.
99US-0125788P.
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03-JUN-1999
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Score: 444.00 Matches: 163 Percent Similarity: 42.55 Conservative: 74 Best Local Similarity: 29.68 Mismatches: 170 Query Match: 13.528 Indels: 150	-09-423-575-1 (1-1886) × AAG14896 (1-533)	303 AATGGACAACAACAACAACACTTTTAGTTCTCTGGAT3	31 AsnGluGlnGlnGlnGlnGlnGln-AlaSerSerSerAsrAlaAlaSerPheSerGl 5	Oy 346ANIGTCATGACCAAAATCCTTCTTCTTGATGGATTTTATACCTTC 392 Db 11eVal8erG1VAsDValArgAsnGluMetValPhalPePrOPr 66	393 AAGAGAATTCAACTTCATTCTCAACAAGACTTCCATGGAA		Qy 453 TCTACAAATGGGTGGCTTTGAATTTTCAATTCTATGCTGACTAACAAATACTT 506	Н	Qy 507 ATCATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTTGAGTTCATGGCTCC 566	Db 102 lSerValSerProPheGlnTyr	CCTC 62	Db 110HisTyrGlnAsnLeuSe 115	QY 627 AAACAACAIGTGGGGTTTTGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGG 686	Db 115 rAshGlnLeuSerTyrAshAshLeuAshPro	Qy 687 TCCAAGTGAACCAATGATGTCTACATTCGGTGAAGATTTCCCGTTTCTAATTTCGAA 746	Db 126 SerThrMetSerAspGlu 131	Qy 747 TAAAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTTTCTGATGATGCTCGGA 806	Db 132AsnGlyLysSerLeuSerValHisGlnHisHisSerAspGlnIleLeuPr 148	IGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAGA : :	Db 148 oSerServalTyrAsnAs 154	Qy 867 CATITCTAATAACGIIGIIIACTCAAGGIIICIC 899	Db 154 nAsnGlyAsnAsnGlyValGlyPheTyrAsnAsnTyrArgTyrGluThrSerGlyPheVa 174	σ	Db 174 lSerSerValLeuArgSerArgTyrLeuLysProThrGlnGlnLeuLeuAspGluValVa 194		spLysGlyGlnAs 214	996 GTCAGGAGCTGCTAGTTCACCTTTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGA 10	214 pPheHisAsnGlySerSerAspAsnIleThrGluAs 226	1056 TGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGAGCATTAGA	226 pAspLysSerGlnSerGlnGluLeuSerProSerGluArgGlnGluLeuGl 243	П	243 IOGUITÁREÁRRARANDE TRANSPORTINA COMBENDARANDE COMBENDA	
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PR 06-AUG-1999; PR 06-AUG-1999; PR 09-AUG-1999; PR 09-AUG-1999;	10-AUG-1999 11-AUG-1999 12-AUG-1999	13-AUG-1999 13-AUG-1999 16-AUG-1999	17-AUG-1999 18-AUG-1999	20-AUG-1999 20-AUG-1999 20-AUG-1999	23-AUG-1999 23-AUG-1999	25-AUG-1999 26-AUG-1999	27-AUG-1999 27-AUG-1999 27-AUG-1999	30-AUG-1999 31-AUG-1999	01-SEP-1999 07-SEP-1999	10-SEP-1999	15-SEP-1999	20-SEP-1999	23-SEP-1999	24-SEP-1999 28-SEP-1999	29-SEP-1999 04-OCT-1999	05-0CT-1999 06-0CT-1999	08-0CT-1999 08-0CT-1999	13-0CT-1999 13-0CT-1999	13-OCT-1999 13-OCT-1999	14-OCT-1999	14-OCT-1999	18-0CT-1999	21-001-1999 21-00T-1999 21-00T-1999	21-0CT-	21-0CT-	22-0CT-	25-OCT-	25-OCT-	26-OCT-	28-OCT-	28-OCT-	Alignment Scores:	Pred. No.:

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The present sequence is Arabidopsis thaliana transcription factor. The transcription factors are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, portato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, carrot, cantaloupe, cauliflower, coffee, cucumber, eggplant, grapes, mango, lettuce, honeydew, melon, onlon, papaya, peas, pepers, pienapple, spinach, caquash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and vegetable brassicas. The transcription factors are specifically useful for modifying traits associated with plant's pathogen tolerance such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, and alterations in the cell death response. Transgenic plants expressing these transcription factors are more tolerant to biotrophic or necrotrophic pathogens such as fungi, bacteria, mollicutes, viruses, nematodes and parasitic higher plants. The transcription factors are also used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ProGlySerSerGlyGlyGlyArgAspLeuAspLeuGlyGlnSerPheArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 ITTATACCTTCAAGAGAATTCAACTTCATTCTCAACAATGCTTCCATGGAATACCATC 441
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e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 GlyGlyllePheAsnPheSerAsnGlyPheAspArgSerAspSerProAsnLeuThrThr
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                                                                                                                                                                                                                                                                                                                Nucleic acids encoding plant transcription factor polypeptides, for altering the pathogen resistance characteristics of plants, corn, potato and cotton plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 ArgileProValTyrGluSerAlaGlyMetLeuSerGluMetPheAsnPhe-
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                                                                                                                                                                                                                 Creelman R,
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                                                                  MENDEL BIOTECHNOLOGY INC.
17-NOV-1999; 99US-0166228P.
17-APR-2000; 2000US-0197899P.
22-AUG-2000; 2000US-0227439P.
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                                                                                HEARD J.
RATCLIFFE O.
CREELMAN R.
JIANG C.
PINEDA O.
REUBER L.
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N-PSDB; AAD06479.
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                                                                                                                                                                                GACTCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAA 1409
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                                                  ACAGITACACACCCGGITTGCCCTCCAAACCGITTCCTTCTTATACAAGAACCTGAGAGA 1292
                                                                                                                                                                                                                                                                                                                                                                                GAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATC 1562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACC 1673
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rHisHisGlnMetGluAlaLeuAlaSerSerPheGluMetValThrGlyLeuGlyAlaAl 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 rSerGlnGlnGlnAsnGlnGlyAsnAsnAsnAsnIleProTyrThrSerAsp-AlaG 476
                                                                                                                                               303 pAlaileLysGluGlnileGlnValIleArgGlyLysLeuGlyGluArgGluThrSerAs
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| OLysGluSerGluLysIleMetLeuSerLysGlnThrGlyLeuSerLysAsnGlnValAl
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500. .560
/note= "Conserved domain"
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688 CCAAGTGAACCAATGATGTCTACATTCGGTGAAGATTTCCCGTTTCTAATTTCGAAT 747 220SerGinThrGluileGlyThrValHisValGluAsnSerGlyGly 234 748 AAAAGAAACAATGACTTCATTGAGTCTTGCATCATTT	GGCTCAAAATAGCTTCACTCGTTCAAAAATACTATCGTCGCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGCCGCATACTCGTCGCCGCATACTCGTCGCTCTCGCCTTCGCCTTCGCTTCACTTCACTTCACGTTCACGTTTTTTTT	AspGlyGlyGlySerSerbroSerSerblaGlyAlaAsnLysTCTACATTTCAAAGGAGAGCATTAGAAGCAAAGAAACCATCTC	TTATATCAGGGTTC	AlaAlaGinSerCysGinLeuLeuGiyAspLysaspAlaAlaGiyIleser ATGGGATCTGTATTGGAGAGAGC	1414 CAGATTGGGGACCTCAACGAGGTTTGCGTTATCGGTTTCGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTTGGTTTTGGTTTT
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3 6 8 6 8 6	6 6 6 6 6	6 6 6 6 6 6	8 6 8 6 8	8 8 8 8 8 8
Disclosure, SEQ ID NO 236; 470pp; English. XX XX XX CC The invention relates to a number of cDNA sequence and their encoded corpore ins which are especially transcription factor cDNAs and their proteins. The isolated or recombinant polynuclectide is useful for producing a modified plant with a modified trait, e.g. enhanced tolerance to environmental conditions, improved tolerance to microbial, fungal or viral diseases, improved tolerance to pest infestation, decreased controllity to take up heavy metals; improved growth under poor photoconditions, improved nutrient uptake, or reduced hormone comprising the desired trait. The polynucleotides and polypeptides are comprising the desired trait. The polynucleotides and polypeptides are comprising the desired trait. The polynucleotides and polypeptides are comprising the desired trait. The polynucleotides and polypeptides are compressed in bioinformatic search methods. This sequence represents one XX Sequence 739 AA;	Alignment Scores: 1.21e-34 Length: 739 Score: 424.00 Matches: 155 Servent Similarity: 41.02% Conservative: 94 Best Local Similarity: 25.54% Mismatches: 171 Cuery Match: 7 Gaps: 24 US-09-423-575-1 (1-1886) x ADE37297 (1-739)	Oy 289 TTCATAGAAACCCAATGGACAACAAC	ilitysGlnGluHisGlnargValGluWetAspGluGl TRACCTTCAAGAGAGTTCAACTTCATTCTCAACAAT 	111	Qy 586

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23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 01-SEP-1999; 10-SEP-1999;	13-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 24-SEP-1999; 24-SEP-1999; 28-SEP-1999; 04-OCT-1999; 05-OCT-1999; 05-OCT-1999;	087-007-1-1099-0	PR 21-0CT-1999; 99US-0160768P. PR 21-0CT-1999; 99US-0160770P. PR 21-0CT-1999; 99US-0160815P. PR 22-0CT-1999; 99US-0160815P. PR 22-0CT-1999; 99US-0160980P. PR 22-0CT-1999; 99US-016098P. PR 25-0CT-1999; 99US-0161404P. PR 25-0CT-1999; 99US-0161406P. PR 25-0CT-1999; 99US-0161406P. PR 25-0CT-1999; 99US-016130P. PR 26-0CT-1999; 99US-016130P. PR 26-0CT-1999; 99US-016130P. PR 26-0CT-1999; 99US-016130P. PR 28-0CT-1999; 99US-0161320P.	ignment Score ed. No.: rcent Similar st Local Simi ery Match: -09-423-575-1 37 A	euGlyGlyValSerGlnMetValGluIleGlnAspSerGlySerTrpArgAspC

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 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 23514.
                                                                                                                                                                                                                                                                                          990S-0121825P.
990S-0123180P.
990S-0125748P.
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                  (first entry)
                                                                                                                                                       Arabidopsis thaliana
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                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                             25-FEB-2000;
                17-OCT-2000
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0y GCTCAAAATACCTTCACGAGAATACTTACCCGGCATACCGCGCGCG	1625 . 373 1673 393 1733	Search completed: September 2, 2004, 12:06:52 Job time : 140.5 secs
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Title:

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1384 CITCITCAGCAGCIGAAACGAAAGAACCATCAGATTIGGAGACCICAACGAGGITIGCCT 1443
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31 SerlleMetSerArgAsnAsnAlaAspThrGlyArgValLeuAlaLeuProGluHis---
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US-09-621-976-4543
US-09-621-976-4543
Sequence 4543, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumes Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TILLE NEFERENCE: GENSET. 054PR2
CURRENT APPLICANTON UNMERR: US/09/621,976
CURRENT FILIG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 142
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CORGANISM: Homo sapiens
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                                                                                                                                   September 2, 2004, 12:02:38 ; Search time 24.5 Seconds (without alignments) 7948.292 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                 protein search, using frame_plus_n2p model
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Db 79 SerGluGluGlu	::: :: ::::	ζŏ	376 AIGGAITITAIACCTICAAGAAGAITCAACTICAITCTCAACAAIGCIICCAIGGAAI 435
Oy 1564 AACTGGTTTATA	AACTGGTTTATAAATGCGCGGGTTAGGAAGCCGATGATAGAAGAG 1614	qq	
Db 99 AsnTrpPhelle	snirpPheileAsnAlaArgArgArgleLeuProAspMetLeuGlnGin 115	λŏ	436ACCATCAGATCAGATCCTCTACAAAIGGGTGGCTTTGATATT 477
RESULT 2 US-09-150-867-1		đ	
<pre>; Sequence 1, Application US/09150867 ; Patent No. 6645748 : GENERAL INFORMATION.</pre>	US/09150867	<u>ک</u> او	478 TICAATICTAIGCTGACAAATACTIAICAICTICCTCCACGGTCIAICGAI 531
; APPLICANT: Wood, Kenneth W APPLICANT: Sakowicz, Roman	h W. man	3 8	
<pre>// APPLICANT: GOLGSTein, Lawrence S.B. // APPLICANT: Cleveland, Don W. // APPLICANT: The December of the Institution // APPLICANT: The December of the Institution // APPLICANT. The December of the Inst</pre>		Db	::: 1998 GluGinileAsnGluAsnValThrThrLeuLys
TITLE OF INVENTION: Plus End-Directed Micr. TITLE OF INVENTION: Chromosome Congression	on the University of California S End-Directed Microtubule Motor Required for omosome Condression	ò	592 CCTTTGGATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGTTTTGAAGCA 651
FILE REFERENCE: 18557C-000110US	000110US BER: US/09/150,867	QQ	2009Glugly 2010
CURRENT FILING DATE: 1998-09-10; EARLIER APPLICATION NUMBER: US	98-09-10 BER: US 60/058,645	δλ	AATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATGATGTCTACA
; EARLIER FILING DATE: 1997-09-11; NUMBER OF SEQ ID NOS: 11	97-09-11 1	셤	2011 GluGlyGluLysGluThrPheTyrLeuGlnArgProSerLysGlnGlnSerSerSer 2029
; SOFTWARE: Patentin Ver.	2.0	ζ	TTTCCC
; LENGTH: 2954 ; TYPE: PRT		QQ Q	2030 GlnMetGluGlu
ORGANISM: Xenopus sp.		ò	772 AGTCTTGCATCAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACA 828
FORMATION: FORMATION:	Xenopus centromere-associated protein-E (XCENP-E) member of the kinesin superfamily of microtubule	Db	2046 GluGluAlaGluLysGluIleSerGluAlaThrAsnGluIleLysAsnLeuThrAlaLys 2065
; OTHER INFORMATION: motor; FEATURE:	motor proteins	δλ	829 AGATTAGCCTCAGAGCTTCTTGCAGCAGCAAAGACATTTCTAATAACGTTGTTACT 888
; NAME/KEY: DOMAIN ; LOCATION: (1). (472) ; TUCCATION: (1). (472)	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	DP	IleSerSerLeuGluGluGluIleLeuGlnAsnAlaSerIleLeuAsnGluAlaValSer
FEATUR NAME/F	בפון דואב וונרכת מסוומווו	<u> </u>	889 CAAGGITTCICAACITATATTTGGCICAAAATACCTTCACTCTCTCTCTCTCAGAAAATACTA 948 ::: 2086 Glu
LOCATION: (473) OTHER INFORMATION	(2752) · . rod domain	8	TOTO BE A SECULD TO SECURD TO SECULD TO SECURD TO SECULD TO SECULD TO SECULD TO SECULD TO SECURD TO SECULD TO SECULD TO SECULD TO SECULD TO SECURD
FEATURE: NAME/KEY: DOMAIN		2 원	
<pre> ; LUCALION: (2/53)(2954) ; OTHER INFORMATION: tail US-09-150-867-1</pre>	4) 1 domain	ò	1009 AGTICAGCCTITACTICACGTITIGAGAATATAACTGAGTITTCTIGATGGTGATTCTAAT 1068
nment Scores:		qq	2112 AspHisAlaPheAlaGlnSerLysArgGluLysAspGluAlaValAsnLysIleAlaSer 2131
		۶ و د	1069 AACTCGGAGGCGTTTCGGATCTACATTTCAAAGGAGAGCAAAGAAAG
st Local Similarity:	Mismatches: Indels:	g &	Demaraciu
DB: 4	Gaps:	qu	::: ::: GluPheArgAspSerLysGluSerLeuGlnGlnGlnSerSerHisLeuSerGluGluLeu 216
CTTT	1 (1 1000) A US-US-IDU-00/1 (1-2934) CTITCACGGAGAAAGAAAAAAAAAAAAAAAAAAAAAAAAA	δλ	1189 CATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGG 1248
1871	nSerLysGlnHisLeuPheSerGlulleGluThr	QQ	2165 CysthrTyr 2172
Oy 196 CACATTTTGGAAA	TTGTCTGAAATCTT	δλ	TTTGCCCTCCAAACCGTTTCCTTCTTATACAAGAACCTGAGAGAGA
 1891 LeuSerLeuSerl	::: :::	da .	
		Qy	1309 ATAATCTCTATGGGATCTGTATTGGAGAGGGAAAGACAAGACTCAAGAAACCTCTATG 1368

; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-861-464-8	Alignment Scores: 0.00271 Length: 1186 Pred. No.: 115.00 Matches: 108 Score: 115.00 Matches: 68 Percent Similarity: 31.77% Conservative: 68 Best Local Similarity: 19.49% Mismatches: 180 Query Match: 3.50% Indels: 198	US: 09-423-575-1 (1-1886) x US-08-861-464-8 (1-1186)	Qy 319 AACAACAACTTTTAGTTCTCTGGATAATGTCATGACTAACCAAAATCCTCTTCTCATG 378 :::	OY 379 GATTITATACCTTCAAGAGAAGATTCAACTTCATTCTCAACAATGCTTCCATGGAATACC 438	Qy 439 ATCAGATCATCTACAAATGGGTGGCTTTGATATTTTCAATTCTATGCTGACTAAC 498	Qy 499 AAATACTTATCATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTTGAGTTC 558	OY 559 ATGGCTCCTCCTCATCCTCCACTTCATCCTTTGGATCATTA 606	OY 607 AGACACTATGATGATTCCTCAACAACAAGGGGTTTTGAAGCAAATAGT 657	Qy 658	Oy 682 GTTGGTCCAAGTGAACCAATGATGTCTACATTGGTGAAGAATTTC 729	Qy 730CCGTTTCTAATTTCGAATAAAGAAACAATGAGCTTTCATTGAGT 774	Qy 775 CTIGCATGAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCA 822 :::::::: Db 845 GlnLeuArgGluIlealaGlyHis1leMetGluPheSerdlnAspGlnHisGlySerArg 864	Qy 823 GCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGGAAGACATTTCTAATAAGGTT 882	Qy 883 GTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTCT 933 ::	OY 934 GITCAAGAATACTATCTCATTTCGCCGCATACTCGATTATTCATCTCGAGGACC 993	Qy 994 GAGTCAGGAGCTAGTTCAGCCTTTACTTCAGGTTTTGAGAATATAACTGAGTTT 1050	OY 1051 CTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGAGCA 1110
	2195 LeuLeudlnHisLeuSerSerLeuLysGludinLeuAspGlulledinMetGlu 22 1429 CAACGAGGT	OY 1450 TCTGTTTCGGTTCTACGGATTGGTTCCAAAACTTCCTTCACCCTTACCCGAAAGAT 1509 :::	Qy 1510 TCGGABAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGG 1569 2249 AspaspvalAlaGluArgMetaspileLeuGluSerArg 2261	OY 1570 TTATAAAIGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAATG 1629 Db 2262AsnGlnGlulleuMetGluLysTleSerAlaValTyrSerGluGln 2279	1630 AAC 1 ::: 2280 His 2	RESULT 3 US-08-861-464-8 Command B Annication IIS/08861464	; Patent No. 5874210 ; GENERAL INFORMATION: ; APPLICANT: Guarente, Leonard P.	APPLICANT: Kennedy, Brian ; TITLE OF INVENTION: Genes Determining Cellular Senescence ; TITLE OF INVENTION: in Yeast , NIMBER OF SECHENCES 16	CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CTRV: Lexington	STATE: MA COUNTRY: USA ZIF: 02173 COUNTRY: OSP	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/861,464 ; FILING DATE: 22-MY-1997 ; CLASSIFICATION: 435	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/396,001 FILING DATE: 28-FEB-1995 PRIOR APPLICATION DATA:	APPLICATION NUMBER: PCT/US94/09351 FILING DATE: 15-AUG-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/107,408	FILING DATE: 16-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Granhan, Particia PROTECTEDITON NIMBER: 32, 227	B 2 2 4	2 4 ⊣

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QD Вþ a ò g g δ Dp δ g ò ò 원장 ò ò 1542 1542 1581 1383 1482 1068 AsnValLeuValLeuSerGlnHisLysPheAlaSerAsnValValGluLysCysValThr 1087 1088 HisAlaSerArgThrGluArgAlaValLeuIleAspGluValCysThrMetAsnAspGly 1107 CGGGTTAGGCTATGGAAGCCGATGATAGAAGAGGATGTATGCGGAAATGAACAAGAGGAAG 1641 1014 1384 CTT------CTTCAGCAGCTGAAAGAACCATCAGATTTGG 1422 |||::::: ||| ------AsnTyrVallleGln 1047 994 GAGTCAGGAGCTGCTACTCAGCCTTTACTTCACGT---TTTGAGAATATAACTGAGTTT 1050 CITGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGAGCA 1110 TTAGAAGCAAAGAAAACCCATCTTGGATCTTCTTCAAATGGTGGATGATCGATATAGT 1170 CAT------TGCGTAGAT-----GAGATTCATACGGTTATATCA 1203 1204 GOGITICCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAAACC 1263 1264 GTTTCCTTCTTATACAAGAACCTGAGAGAGAATCTGCAAGAAGATAATCTCTATGGGA 1323 925 ValleuSerLeuAlaLeuGlnMetTyrGlyCysArgValIleGlnLysAlaLeuGluPhe 944 PhePheGluPheGlySerLeuGluGlnLysLeuAlaLeuAlaGluArglleArgGlyHis 924 ------ArgGlu 956 GCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAAGACATTTCTAATAACGTT 882 934 GITCAAGAAATACTATCTCATTTCGCCGCATACTCGCTCGATTATTCATCTCGAGGAACC 993 -TIGACAAGAAGICAGGIAICAAACIGGIITAIAAAIGCG ||||::: ::::|||::: ----ATATTTGGCTCAAAATACCTTCACTCT TCTGTATTGGAGAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCATTGC 1423 AGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAA ---CACCCTTACCCGAAAGATTCGGAGAACATCTTCTAGCTATACGAAGT GlnLeuArgGluIleAlaGlyHisIleMetGluPheSerGlnAspGlnHisGlySerArg ::: IlevalMetHisLysIleArgProHisIleAlaThrLeuArg 1152 CTCAATAACAGTCACATTCAACCCAACGACCAACTCTTCGA 1683 ::: 945 IleProSerAspGlnGlnAsnGluMetVal-------GITACTCAAGGITICTCTCAACTT----992 ÁlaPheLysGlyGlnVal-----1003 HisProTyr-.540 GGC----1483 1108 1582 1642 1139 1324 1542 1543 1126 1051 1111 1111 823 865 883 원 장 원 δ 셤 음성음 6 B 6 g QY Db

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GITGGICCAAGTGAACCAATGATGTCTACA------TTCGGTGAAGAAGAITTC 729 AIGGCICCICCICCICCICCICCICCACTICAI ------CCITIGGAICAITIA 606 ----CCGTTTCTAATTCGAATAAAAGAAACAATGAGCTTTCATTGAGT 774 319 AACAACACTITIAGTICICIGGATAATGICAIGACTAACCAAAAICCTCTICICAIG 378 |||| |||||| ||||||| ::: ||||::: |||| ------SerArgArgAspSerLeuThrGlySerSerAspLeuTyrLysArgThr AAATACTTATCATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTTGAGTTC ---GAGTTTCAGGCATTTTCAGGTGTA 379 GATTITATACCTTCAAGAGAAGATTCAACTTCATTCTCAACAATGCTTCCATGGAATACC 439 ATCAGATCAGATCCTCTACAAATGGGTGGCTTTGATATTTTTCAATTCTATGCTGACTAAC APPLICANT: Quarente, Leonard P.
APPLICANT: Quarente, Leonard P.
APPLICANT: Quarentaco Jr., Nicanor
APPLICANT: Claus, James J.
APPLICANT: Claus, James J.
APPLICANT: Claus, James J.
APPLICANT: Claus, James J.
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YEAST
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050,1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-02-29
PRIOR FILING DATE: 1994-08-15
PRIOR FILING DATE: 1994-08-15
PRIOR FILING DATE: 1994-08-15
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1186
TYPE: RATE APPLICATION OF APP AGACACTATGATGCTCCAAACATGTGGGGGTTTTGAAGCAAATAGT ---SerPheSerSerSrProGlyProValGlyMet-------H 1186 108 68 180 198 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-423-575-1 (1-1886) x US-09-323-433A-8 (1-1186) RESULT 5
US-09-233-433A-8
IS-09-233-433A-8
> Sequence 8, Application US/09323433A
> Patent No. 6218512
; GENERAL INFORMATION: AshSerAshThrGlySerGly---0.00271 115.00 31.77% 19.49% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: 607 785 869 705 721 736 559 747 658 730

735 558 681

qq	825 MetProSerGlyArgSerArgLeuleuGluAspPheArgAsnAsnArgTvrProAsnLeu 844	Db 1126GlnLysMetIleAspValAlaGluProGlyGlnArgLys 1138
Š		Qy 1642 CTCAATAACAGTCACATTCAACGCAACGGACCAACTCTTCGA 1683
² 원	pGlnHisGlySerArg 864	Db 1139 IleValMetHisLysIleArgProHisIleAlaThrLeuArg 1152
ζ O	8882	RESULT 6 US-09-134-001C-4318 Sequence 4318, Application US/09134001C , Patent No. 6380370
oy do	883 GTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTCT 933 :::	; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS ; TITLE OF INVENTION: EPIDERVIDIS FOR DIAGNOSTICS AND THERAPRITICS
Qy Dp	£ 66	FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
& £	GAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCACGTTTTGAGAATATAACTGAGTTT 1050	FAILOR FILLING DATE: 1997-11-08 PRIOR PILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14
8 6	CTIGATGGTGATTCTAATAACTCGGAGGGGGGTTTCGGATCTACATTTCAAAGGAGGCGTT110	MONDER OF SET ID NOS: Set 18 LENGTH: 676 TYPE: PRT
· & 8	TRAGAAGCAAAGAAAACCCATCTCTTGGATCTTCTAAATGGTGGATGATCGATAGATGGTTGATAGT 1170	Staphylococcus epiderminus -4318 -es:
ò a	CATTGCGTAGATGAGATTCATACGGTTATATCA 1203 H H H H H H H H H H	Score: 114.50 Matches: 79 Percent Similarity: 36.75% Conservative: 75 Percent Similarity: 18.85% Mismatches: 140
ે ઇ	GCGTTCCATGCTGCAACCGAGTTAGATCCACACCCGGTTACACACCCGGTTTGCCCTCCAAACC 1263	Gaps: 9-134-001C-4318 (1-676)
i ò	GITICCTICITATACAAGAACCIGAGAGAGAAATCIGGAAAGAAAAATCICTAIGGGA 1323	Qy 280 AGGATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAACACTTTTAGTTCT 339
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DP Qy	1017	400 GAITCAACTICATCTCAACAATGCTICCATGGAATACCATCAGATCCATCAAA 45
⊋ qa Xo	1018 LeuProAspGlnThrLeuProIleLeuGluGluLeuHisGlnHisThrGluGlnLeuVal 1037 1423 AGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTGGGTTCTACGGAATTGGATGTTCCAA 1482	Db 332 AspAsn
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업	HisAlaSerArgThrGluArgAlaValLeuileAspGluValCysThrMetAsnAspGly 1107	368
۶ ج د	1543TIGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCG 1581	<pre>Qy 700 ATGATGTCTACATTGGGGAAGATTTCCGGTTTCTAATTTCGAAT 747 </pre>
ò	CGGGTTAGGCTATGGAAGCCGATGATAGAAGATGATGCGGAAATGAACAAGAGGAAG 1641	Qy 748 AAAACAARGAGA-AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA

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Sequence 10. 6175000
GENERAL INFORMATION:
APPLICANT: Canas, Glen A. APPLICANT: Diabali, Malek APPLICANT: Diabali, Malek APPLICANT: Salleri, Licia APPLICANT: Salleri, Licia APPLICANT: Tarry, Pauline TRILE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23 TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 GACAAGACTCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGA 1404
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|----ProSerLeuLeuAspArgIleAsnLys 582
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                                                                                                                                                           512 IleAsnLysAspLysAlaLysIleIleAlaAspValIleAlaArgValGlnLysAspLys 531
                        B68 ATTICTAATAACGITGITACTCAAGGITTCTCTCAACTTATATTTGGCTCAAAATACCTT 927
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                                                                ATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAAGAGAC 867
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444 South Flower Street, Suite 2000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2483 rasplysileGlyAspLysGlyLeuSerMetProGlyValProLysAlaProProMetGl 2503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2503 nvalGluģiyseralalysGluLeuGlnAlaProArgLysArgThrValLysValThrLe 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATAAATAAGCATTATCTTCTTCTGGTTTTTAACACACATTTTGGAAATTTTGATGTA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 AAAATTCTCTTTGGAACGTTGTTGTCTGGAAATCTTCCCAAAGGTTCTATCAGAAGAAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AAGGATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAACAACAACAACTTTTAGTTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 TCTGAATCTTTTAGTGAGGCAGATGATGAAGATTATGAATTTCTTCATGAAATTATTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AACCAAAATCCTCTCTCATGGATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 ACCITCAAGAGAATTCAACTICATICTCAACAATGCTTCCATGGAATACCATCAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SerSerSerArgAspArgArgGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AsnArgSerSerIlelleAsnGluHisMetGly-----
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Matches:
Conservative:
Mismatches:
Indels:
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MATION DATA:
UMBER: US/08/061,376
13-MAY-1993
                                                                                                                                            9387
       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,3'
FILING DATE: 13-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Refer, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 41 931
TELECOMMUNICATION INFORMATION:
TELEFAX: (619)546-4937
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3969 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGGATAATGTCATGACT
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19.88%
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                                                                                                                                                                                                                                                                                  ; STRANDEDNESS: unknowr TOPOLOGY: unknown , MOLECULE TYPE: protein US-08-061-376-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 AATGGGTGGC-
                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2399
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DB:
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Oy 1644 CAATAACAGTCACATTCAACCCAACGGACCAACTTCGAAGTGCCAAAATCTGTTATGAT 1703	80 yrileLeuLysGlyllelleThrPro 488 81E-5 5, Application US/08194981E 1. S886157 1. NPORMATION: 1. ANT: GUENGERICH, F. Peter 1. ANT: GUENGERICH, P. Peter 1. ANT: GUENGERICH, P. Peter 1. ANT: GILLAM, Elizabeth M. J.	TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF TITLE OF INVENTION: HUMAN TITLE OF INVENTION: HUMAN TITLE OF INVENTION: CYTOCHROME P450 NUMBERS OF SEQUENCES: 68 CORRESPONDENCE ADDRESS: ADDRESSEE: Nation & ROSENBERG, P.C. STREET: Suite 1200, 127 Peachtree Street, NE CITY: Atlanta STATE: Georgia COUNTRY: USA STATE: Georgia COMPUTER READABLE FORM: MEDIUM TYPE: Flogpy disk MEDIUM TYPE: Flogpy disk COMPUTER PRADABLE FORM:	CORRACTING SYSTEM: PC-DOS/MN-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURSENTING SYSTEM: PC-DOS/MN-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURSINICATION NUMBER: US/08/194,981E FILING DATE: February 10, 1994 CLASSIFICATION: 435 ATTCRNEY/AGRAT INFORMATION: NAME: Elizabeth Selby REGISTRATION NUMBER: 2200.0022 TELEPHONE: (404) 688-0770 TELEPHONE: (404) 688-980 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:	JENGTH: S12 amino acids JENGTH: S12 amino acids
	TTGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1095 ATTTCAAAGGAAGCAATAGAAAGAAAAAAAAAACCCATCTTGGATCT 1142 206 ePheLysLysGluValleuAspArgLeuAsnSerGlyMetHeAspLysLeuTyrPheLe 226 1143 TCTTCAAATGGTGGATGATGATATAGTCATTGCGTAGATCATACGGTTAT 1199 1143 TCTTCAAATGGTGGATGATCATATAGTCATTGCGTAGATCATACGGTTAT 1199 1250 uLeuLysIleCysLysGluAsnPheProAlaThrSerValLysAspValGlnLysGluPh 246 1200 ATCAGCGTTCCATGCTGCAACCGAGTTAGATCACACCCGGTTTGCCT 1256 121	259SerValAspileHeuArgProAshieldProileCySArgGiuGinArgil 275 1317 TATGGATCTGTATTGGAGAGAGGCAAAGACAGAGACAGAGAACCTCTAT 1367 ::::::::	331 uLysIleLeuTyrSerLeualaPheAlaArgAsnLysLeuTyrAsnGlyPheLeuAsnPh 351 1495

us-09-423-575-1.rai

		CAGCTGAAACGA	Oy, 1465 CGGAATTGGATGTTCCAAAACTTCCTTCACCCGAAAGATTCGGAGAAACAT 1521 152	Oy 1558 GTATCAACTGGTTTATAATGCGCGGGTTAGGAGCCGATGAAGAGAGATG 1617	RESULT 13 US-08-918-190-2 ; Sequence 2, Application US/08918190 ; Patent No. 6072031 ; GENERAL INFORMATION: ; APPLICANT: Pastan, Ira ; APPLICANT: Brinkmann, Ulrich ; TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY ; TITLE OF INVENTION: PROTEIN (CSP) AND ANTISENSE CSP	CORRESPONDENCES: 10 CORRESPONDENCESS: STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA COUNTRY: USA ZIP: 92660	COMPUTER READBLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: IBM Compatible COMPUTER: IBM Compatible COMPUTER: IBM COMPATE: COMPUTER: SOFTWARE: FastEGO Version 1.5 CURRENT APPLICATION DATA: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/480,662 FILING DATE: 07-JUN-1995
Query Match: 3.24\$ Indels: 177 DB: 1 Gaps: 26 US-09-423-575-1 (1-1886) x US-08-480-662-2 (1-971) QV 181 CTTCAGTTTTTAACACACATTTTGGAAATTTTGATGAAAAATTCTCTTTGGAAGGTTGT 240 DD 8 LeuGlnThrLeuThrGluTyrLeu	21	DD 40 GIRASRITYFFOLEULEULEULEULEUGIULYSSERGIRASPASRVAIIIELYS 59 QY 403TCAACTTCAACAAGACTTCCTAACAATGCTTCCATGGAATACCATCAGTCA 447 E:	487 AIGCTGACTAACAATACTTATCATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGC 54	DD 114 AlalleSerlielleGlyArgGluAspFhebro	OY 727 TTCCCGTTTCTAATTTCGAATAAGAAACAATGAGCTTTCATTGATCTTGCATCAGAT 786 Db 164PheLysSerAsnGluLeuTrpThrGluileLysLeuValLeu 177 OY 787 GTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGAA 846 178AspAlaPheAlaLeuProLeuThrAsnLeuPheLysAlaThrIleGluLeu 194	847 GCTTCTGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTCTCAACTT 11	Oy 967 TCGCTCGATTATTCATCTGAGGAACCGAGTCAGGAGCTGGTTCAGTTCAGCTTTACTTCA 1026 Db 222

164	ABSUL 14 US-09-234-232-2 ; Sequence 2, Application US/09234232
ATTOCANY / ALBYT INPORMATION:	Oy 727 ITCCCGTTTCTAATATAAAAAAAAAAAGAATGAGCTTTCATTGAGTCTTGCATCAGAT 786

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

ITILE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          971
1117
74
1193
1177
                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOSTWARE: FRACESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,232
FILING DATE: 20-Jan-1999
CLASSIFICATION: <UNANDAMA:
APPLICATION NUMBER: US/09/234,232
FILING DATE: 40-Jan-1999
CLASSIFICATION: <UNANDAMA: STATORNEY/AGENT INFORMATION:
NAME: ISRAEISEN INFORMATION:
NAME: ISRAEISEN NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
TELLEPAK: 619-235-0176
TELLEPAK: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                         TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0207
106.50
34.05%
20.86%
3.24%
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-234-232-2
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ATCTGCAAGAAGATAATCTCTATGGGATCTGTATTGGAGA-------GAGGCAAA 1344 .027 CGTITICAGAATAIAACIGAGITICTTGATGGIGATTCTAATAACTCGGAGGCGGGTTTC 1086 GATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTTATATCAGGGTTCCATGCT 1215 GCAACC-----GAGTTAGATCCACAGTTACACCGGTTTGCCCTCCAAACCGTTTCC 1269 1087 GGATCT-----ACATTTCAAAGGAGGCATTAGAAGCA------AAGAAAACCCAT 1131 |||||||::||||||| LeuleuGlubeuLeulysSerGlnIleCysAspAsnAlaAlaLeuTyrAlaGlnLysTyr 282 ::: SerValCysGluArgProHisTyrLysAsnLeuPheGluAspGlnAsnThrLeuThrSer 342 ||||:::::::: |||||| :::|||:: | AsnPheGlnAspLeuProGluPheTrpGluGlyAsnMetGluThrTrpMetAsnAsnPhe ||||::: ::: ::: AspGluGluPheGlnArgTyrLeuProArgPheValThrAlaileTrpAsnLeuLeuVal --TACAAGAACCTGAGAGAG-CTCTTGGATCTTCTT-----TTCTTA----223 1132 263 1156 1216 1270 243 283 222 323

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CTTCAGITITIAACACACATITIGGAAAITITIGAIGIAAAAAITCTCTTIGGAACGIIGT 240

US-09-423-575-1 (1-1886) x US-09-234-232-2 (1-971)

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Percent Similarity: Best Local Similarity: Query Match: DB:

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101 CCAATGGACAACAACAACAACAACACTTTTAGTTCTCTGGATAATGTCATGACTAAC 360

241 GTTGTCTGAAATCTTCCCAAAGGTTCTATCAGAAGAAGAAGAAGATAAAAGTTTCATAGAAAC

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33

361 CAAAAT-----CCTCTTCTCATGGATTTTATACCTTCAAGAGAAGAT------ 402

967 ICGCICGAITALICAICICGAGGAACCGAGICAGGAGCIGCIAGIICAGCCTITACIICA 1026

|||| |IleLeuIleSerLysLeuPheTyrSerLeu-----

213

787 GITTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAA 846 ::: |||| |-----AspAlaPheAlaLeuProLeuThrAsnLeuPheLysAlaThrIleGluLeu 194

727 ITCCCGITTCIAATTTCGAATAAAAGAACAATGAGCTTTCATTGAGTCTTGCATCAGAT 786

164

178

GCATTITCAGGIGIAGIIGGGICCAAGIGAACCAAIGAIGICIAACAITCGGIGAAGAAGAI 726

547 AAIGITGAGITCAIGGCICCICCICCICAIÇÇICCICCACTICAICTITGGAICAITIA 606

100 MetLeu----

486

--TGGAATACCATCAGATCA

:::||| :::::: GluProAsnLysIleCysGluAlaAspArgValAlaIleLysAlaAsnLleValHisLeu

GATCCTCTACAAATGGGTGGCTTTGAT-

148 80 187 AIGCIGACIAACAAAIACIIAICAICIICICCACGGICIAICGAIGIICAAGAIAACCGC

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603

AGACACTATGATTCCTCAAACAACATGTGGGGGTTTTGAAGCAAATAGTGAGTTTCAG 666

Alignment Scores: Prof. No.: 106.50 Matches: 117 Percent Similarity: 34.05\$ Mismatches: 74 Mismatches: 193 Query Match: 3.24\$ Indels: 5 US-09-423-575-1 (1-1886) x PCT-US96-09927-2 (1-971)	QY 181 CITCAGITITIAACACACATITIGAAATITIGAAAAITCTCTTIGGAACGIIGT 240 DD	OY 241 GITGICIGAAAICITCCCAAAGGITCIATCAGAAGAAGAAGAAGAITCAIAGAAAC 300	Qy 301 CCAATGGACAACAACAACAACAACATTTTAGTTCTCTGGATAATGTCATGACTAAC 360 Db 33	Qy 361 CAAAATCUTCTICTCAIGGATTTTAIACCTTCAAGAGAAGAT 402	QY 403TCAACTTCATAAGAATGCTTCCATGGAATACCATCAGATCA 447 ::: :::	QY 448 GATCCTCTACAAATGGGTGGCTTTGAT	QY 487 AIGCTGACTAACAAATACTTATCATCTTCTCCACGGTCTATCGAIGTTCAAGATAACCGC 546	OY 547 AAIGITGAGITCAIGGCICCICCICCICCAICCICCACCITCAICCITIGGAICAITIA 606 114 AlaileSerileileGlyAkgGluAspPhePro124	Oy 607 AGACACTATGATTCCTCAAACATGTGGGGGTTTTGAAGCAAATAGTGAGTTTTCAG 666 :::	Qy 667 GCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATGATGTCTACATTCGGTGAAGAT 726	Qy 727 TICCCGTITCTAATITCGAATAAAAGAAACAAIGAGCTITCATIGGGTCTTGCATCAGAT 786	QY 787 GTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAA 846	Qy 847 GCTTCTGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTCTCAACTT 906	QY 907 ATALTIGGCTCAAAATACCTTCACTCTTCAAGAATACTATCTCATTTGGCGCATAC 966	967 TCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCA	Db 222	Qy 1027 CGTTTGAGAATATAACTGAGTTTCTTGATGGTGATACTCAATAACTCGGAGGCGGGTTTC 1086
GACAAGACTCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTCAGCAGCTGAAACGA 1404 :: ::: ::: ::: ::: ::::	1717415 110 AAGTCAG 1557 :::: Aeralaa 430	GGTTAGGCTATGGAAGCCGATGATAGAAGAGATG 1617	CARIAACAGTCACATTCAACCCAACGGACCAAC 1676	701 1000101101101110111011011011011011011	Represented by the of Health and Human	LUTLAR APOPTOSIS SCEPTIBILITY PROTEIN (CSP) AND ANTISENSE CSP	Olson and Bear Drive 16th Floor		le ion 1.5	T/US96/09927 95	, , , , , , , , , , , , , , , , , , , ,	655 NIH112.001QPC DN:	550	1.d8s			
Qy 1345 GACAAGACTCAAGG Bb 362 heGluAspAsnSe; Qy 1405 AAGAACCATCAGA Qb 375GluGlySerAs; Qy 1465 CGGAATTGGATGT Db 394 vsiysphe	1522	1558	1618	RESULT 15 PCT-US96-09927-2	GENERAL INFORMATION: APPLICANT: The United States, As APPLICANT: Secretary, Department	VENTION: VENTION: EQUENCES:		R 4:	MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1	CACKENT AFFILTATION DATA: APFILCATION NUMBER: PC FILING DATE: 07-JUN-19 CLASSIPTCATION: DELO ADDITION:	APPLICATION DAIS: STILING DATE: 07-JUN-1995 ATTORNEY/ABBYI INFORMATION: NAME: 1-2-2-3	REGISTRATION NUMBER: 29,65; REFERENCE/DOCKET NUMBER: N: TELECOMMUNICATION INFORMATION	ILLEFONE: 019-235-0350 TELEFAX: 619-235-0176 TELEX: INFORMATION FOR SEQ ID NO:	SEQUENCE CHARACIERLEIICS: LENGTH: 971 amino acids TYPE: amino acid STRANDEDNESS: single	; TOPOLOGY: linear; ; MOLECULE TYPE: peptide ; HYPOTHETICAL: NO	; ANTI-SENSE: NO ; FRAGMENT TYPE: N-terminal	60

Search completed: September 2, 2004, 12:14:17 Job time : 64.5 secs

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us-09-423-575-1.rapb

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RESULT 1

US-10-444-599-273470

US-10-444-599-273470

Deblication No. US20040031072A1

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwa K

APPLICANT: Cao Yongwa K

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 273470

LENGTH: 702
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                    Sequence 37653, A Sequence 2365, App Sequence 26821, App Sequence 56821, App Sequence 122156, Sequence 110193, Sequence 180416, Sequence 43080, A Sequence 48619, A Sequence 48619, A Sequence 193114, Sequence 208750,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CTHER INFORMATION: Clone ID: PAT_MRT3847_88966C.1.pep
US-10-424-599-273470
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US-10-425-164-3763
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US-10-425-114-37027
US-10-425-114-37028
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ORGANISM: Glycine
     Alignment Scores
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415.5
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          Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlh
-De/Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlh
-De/Command line parameters:
-Qe/Cogn2 1/USPTO_Eppool/USO942357/runat 01092004 161109_18704/app_query.fasta_1.2055
-De-Published Applications AA -QFWT=fastan -SUFFIX=rapb -MINNARCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-humard-0.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFWT=00 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFWT=0 -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=USO9423575 GCGN 1, 1 161 @runat 01052004 161109_18704
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                        9; Search time 332.5 Seconds (without alignments) 3574.213 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                      atttagttataaaatgttgc..........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/NCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*
                                   version 5.1.6
- 2004 Compugen Ltd
                                                                                                                              - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
, Fgapext
, Delext
                                GenCore
Copyright (c) 1993
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seq length: 200000000
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1 atttagttataaaa
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Perfect score:
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Maximum DB
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No.
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Qy 1324 TCTGTATTGGAGGGAAAGACAAGACTCAAGAAACCTCATG 1368 Db 339 LysThrLeuGIGLWSpAspCysLeuGlyValLysValGluGlySerArgLeu 356 Qy 1369TTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACAAAGAC 1410 Db 357 ArgTyrValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnLeuGlyMetIleGln 376 Qy 1411 CATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAACTTTGGGTTCTACGGAAT 1470 Db 377 ProAsnAlaTTGAGACCTCAACGAGGTTTGCCTGAGAAACTTTGGGTTCTACGGAAT 1470 Cy 1471 TGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCT 1530 Cy 1471 TGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTCTAGCT 1530 Db 397 TrpLeuPheGluHisPheLeuHisProTyrProLysAspSerAspLysValMetLeuAla 416 Cy 1531 ATAGGAAGGTTGACCAGTATCAACTGGTTTATAAATGCGCGGTTTAGG Cy 1611	Oy 1591 CTATGGAAGCCGATGATAGAAGAGATGATGAAGAGAGAAATGAACAAGAGAATAAC 1650 by 437 LeuTrpLysProMetValGludluMetTyrLeuGludluIleLys	APPLICANT: Liu, Jingdong APPLICANT: Liu, Jingdong APPLICANT: Avoil's David K. APPLICANT: Screen, Steven E. APPLICANT: Screen, Jack E. APPLICANT: Tabaska, Jack E. APPLICANT: Tabaska, Jack E. APPLICANT: Tabaska, Jack E. APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 LENGTH: 550 LENGTH: 550 TYPE: PRT CORGANISM: Zea mays)RMATION 37053 es: rrity: hilarity	US-09-423-575-1 (1-1886) x US-10-425-114-37053 (1-550) QY
2.24e-40 Length: 702 503.00 Matches: 143 milarity: 44.97% Conservative: 58 milarity: 31.99% Mismatches: 142 15.32% Indels: 104 15.32% Indels: 104 15.32% Indels: 104 AACCGCAATGTTGAGTTCATGGTTCCTCCTCCTCCTCCTCTCTTTGGAT	682 106 688 126 721 146	781 166 841 173 901 190 961	QY 985 CGAGGAACCGAGTCGTAGTTCAGCCTTTACTTCAGGAATATAACT 1044 Db 230 GluSerThrAsnSerGlyAlaAlaGlyAspGlyGly	Oy 1147 CARATGGTGGATGATCGATATGCGTAGATGATCATACGGTTATATGAGG 1206

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-ACTCTTCGAATG 1686
                                                                 467 GluLysThrProLeuAspGlnSerAsnGluAspSerAlaSerLysSerThrSerAsnGln 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAACAACAACATTTTAGTTCTCTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yu, Guo-Limata
APPLICANT: Yu, Guo-Limata
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERNCE: MBI-0047
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR PILICATION NUMBER: 09/837,944
PRIOR PAPLICATION NUMBER: 00/310,847
PRIOR PAPLICATION NUMBER: 00/310,847
PRIOR PAPLICATION NUMBER: 00/310,847
PRIOR PLING DATE: 2001-08-22
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR PLING DATE: 2001-11-1
PRIOR APPLICATION NUMBER: 00/336,049
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-09
PRIOR PLING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR PILING DATE: 2002-08-09
                                                                                                               1687 CCAAAATCTGTTATGATGAGCCAAGCAATGCATAAATAAGACAACAAT 1734
                                                                                                                                                           487 GluLysSerProMetAlaAspThrAsnTyrHisMetAsnProAsnHis 502
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1152
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119
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                  ; Sequence 2672, Application US/10374780A; Publication No. US20040019927A1
                                                                                                                                                                                                                                                                                                                 APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reuber, T. Lynne
Keddie, James
Broun, Plerre E
Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                   Creelman, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2906
SOFWARE: Patentin version 3.2
SEQ ID NO 2672
LENCTH: 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.61e-37
472.00
42.01%
28.25%
14.37%
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Adam, Luc J
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US-10-374-780A-2672
                        1663 CCCAACGGACCA-
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity:
                                                                                                                                                                                                                               US-10-374-780A-2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       994 GAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCACGTTTTGAGAATATA---ACTGAGTTT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ACATTTCAAAGGAGGAGTTTAGAAGCAAAGAAA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1126 ACCCATCTCTTGGATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1186 ATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTA---GATCCACAGTTACAC 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1423 AGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTICCTTCACCCTTACCCGGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGC 1542
                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| :::::||| ::::
273 AlaLysLeuSerAsnMetLeuHisGluValGluGlnArgTyrArgGlnTyrHisGlnGln 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCG 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGATAGAAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAA 1662
                                                                                iii
147 GlnGlnGlnGlnGlnHisHisGlnGlnHisGlnProIleHisValGlyPheGlySer 166
                                                                                                                                       813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ProValGlyGluSerSerAlaGlyAlaGlyGlyGlyGlyGlyGlyGlyAlaGluAla 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 AlaGlyLysArgProValGluLeuGlyThrAlaGluArgGlnGluIleGlnMetLysLys 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||
| ArgGlnGlnArgAlaLeuGlnGlnLeuGlyMetIleGlnHisProSerAsnAsnAlaTrp 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAlaAlaAsGluThrProArgAlaGlnGlnGlyLeuSerLeuThrLeuSerSerGln 146
                                                                                                                                                                                                                               814 CITIGIGCAGCIACAAGATIAGCCICAGAGCAAGCIICTIGCAGCAGCAAGACAITICI 873
                                                                                                                                                                                                                                                                             -----GlySerThr 179
                                                                                                                                                                                                                                                                                                                        874 AATAACGTTGTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTCT 933
                                                                                                                                                                                                                                                                                                                                                                 180 GlySerGlyValThrAsnGlyIleAlaAsnLeuVal---SerSerLysTyrLeuLysAla 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspMetAsnAlaLysSerGlnLeuPheSerSerLysLysLysGlySerCysGlyAsnAspLys 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 SerValSerGlyValGlyArgPheGluGlySerArgLeuLysPheValAspHisHisLeu 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAACCAATGATGTCTACATTCGGTGAAGAATTTCCCGGTTTCTAATTTCGAATAAAGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                -----CTGAAACGAAAGAACCATCAGATTTGG
                                                                                                                                     754 AACAATGAGCTTTCATTGAGTCTTGCATCATGTTTCTGATGAATGCTCGGAGATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051 CTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AladindiuLeuLeuAspGluValValAsnAlaAspSerAsp-----
                                                                                                                                                                                167 GlyHisGlyGluAspIleArgValGlySer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1387 CTTCAGCAG-----
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8 8 8 8 8 8 8	8 6 8 6 8 6 8 6 8	8 6 8 6 8 6 8 6 8 6	8 6 8 6 8 6 8 6

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NS-10-425-114-56821
Sequence 5821, Application US/10425114
Subblication No. US2004003488841
Subblication No. US2004003488841
Subblication No. US2004003488841
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Acvan E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Nucleic Acid Molecules (or Plant Improvement)
TITLE OF INVENTION: Nucleic Acid Molecules (or Plant Improvement)
TITLE OF INVENTION: Nucleic Acid Molecules (or Plant Improvement)
TITLE OF INVENTION: Number: 126/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                              CCCAACGGACCA-----ACTCTTCGAATG 1686
1363 TCTATG-----TTCCACCAGCATTGCCTT 1386
                                                                         ----CTGAAACGAAAGAACCATCAGATTTGG 1422
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                               347 ServalSerGlyValGlyArgPheGluGlySerArgLeuLysPheValAspHisHisLeu 366
                                                                                                                                                                             407 HisPheLeuHisProTyrProLysAspSerAspLysHisMetLeuAlaLysGlnThrdly 426
                                                                                                                                                                                                                                                                                                                                                                                                                     467 GlulysThrProLeuAspGlnSerAsnGluAspSerAlaSerLysSerThrSerAsnGln 486
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                                                                                                     1423 AGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAA
                                                                                                                                                                                                                                    1483 AACTICCTICACCCTIACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGC
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US-10-425-114-56821
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Query Match:
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ORGANISM: Zea mays
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Score: Percent Similarity: Percent Similarity: 45.90% Conservative: 56 Best Local Similarity: 11.24% Mismatches: 98 Query Match: 16 Gaps: 10 US-09-423-575-1 (1-1886) x US-10-437-963-122156 (1-594) Qy 757 AATGAGCTTTCATTGATTGATTGATTGTTTCT	Qy 793GATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCT 849	Qy 850 TCTTGCAGCAGCAACATTCTAATAACGTTGTTACTCAA	OY 892GGTTTCTCTCAACTTATATTTGCCTCAAAATACCTTCACTCT 933	Qy 934 GTTCAAGAAATACTATCTCTTTC	OY 958GCCGCATACTCGCTCGATATTCATCTCGAGGAACCGAGTCAGGAGCTGCT 1008	Oy 1009 AGTHCAGCCTTTACTTCACGAATATAACTGAGTTTCTTGATGGTCATTCTAAT 1068 Db 291 GlyGlyAlaProSerSerAlaValSerSerAsnAsnGlnLeulleAlaSerSerGlyGlu 310	OY 1069 AACTCGGAGGGGTTTCGGATCTACATTTCAAAGGAGAGCATTAGAAGCAAAGAAAACC 1128	QY 1129 CATCTCTTGGATCTTCTTCAAATGGTG	00 00 00 00 00 00 00 0
GATTGGT	1207 TTCCATGCTGCAACCGAGTTAGATCCACAGTTACACCCGGTTTGCCCTCCAAACC 1263	1264 GTTTCCTTCTTATACAAGAACCTGAGAGAACAACAACAAGAACATAATCTCTATGGGA 1323 	1324 TCTGTATTGGAGAGGCAAAGACAAGACTCAAGAACCTCT	1366	1402 CGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTT 1461 	1462 CTACGGAATTGGATGTTCCAAAACTTCCTTCACCCTACCCGAAAGATTGGGAGAACAT 1521	1522 CTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCG 1581 ::: :::::	1582 CGGGTTAGGCTATGGAAGCCGATGATAGAAGATGTATGCGGAAATGAACAAG 1635 	RESULT 7 US-10-437-963-122156 Squence 12156, Application US/10437963 Fublication No. US2040123343A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Mu, Wei APPLICANT: Mu, Wei APPLICANT: Buckharcv, Andrey A. APPLICANT: Buckharcv, Brad APPLICANT: Buckharcv, Brad APPLICANT: Buckharcv, Andrey A. FILE REFERENCE: 38-21(51221) CURRENT APPLICANT: Bloomer A. NUMBER OF SEQ ID NOS: 204966 IENGTH: S94 TYPE: PRT CURRENT PROMMATION: Clone ID: PAT_MRT4530_2510C.1.pep Alignment Scores: Alignment Scores:

	Db 224 GlnAlaAlaAlaAlaGlvAlaGlvAlaAlaLeuPheHisProThHisGlvAspAspAla 243
Qy 1486 TICCTICACCCTIACCCGAAAGATICGGAGAAACAICTICTAGCIATACGAAGIGGCTIG 1545	OLU
Db 506 PheLeuArgFroTyrFroLysAspSerGluLysGluMetLeuAlaAlaArgSerGlyLeu 525	
Qy 1546 ACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGAGCCGATG 1605 .::	OY 898 TCTCAACTTATATTTGGCTCAAAATACCTTCACTCTGTTCAAGAAATACTATCTCAT 954
Qy 1606 ATAGAAGATGTATGCGGAAATGAACAAG 1635 Db 546 IleGluGluMetCysGluGluLeuLysAzg 555	Qy 955 TTCGCCGCATACTCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGA 1002
RESULT 8 US-10-437-963-110193	1003 GCIGCIAGITCAGCCITIACITCACGITITGAGAATATAACIGAGTITCITGAIGGIGAT
; Sequence IIV193, Application US/1043/963 ; Publication No. US20040123343A1	304 GluAlaSerGlnAla
; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K.	<pre>Qy 1063 TCTAATAACTCGGAGGGTTTCGGATCTACATTTCAAAGGAGA</pre>
	1108GCATTAGAAGCAAAGAAAACC11
; AFFLICANT: BOUKNAIOV, Andrey A. ; AFFLICANT: Barbazuk, Brad . abbircant: 1: bind	DD 337 GLYGLYALAALASerGluGluAlarnrrrolnrGLYGlurneLeuAlaGlurheLeuval 356
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement	357 GluHisLeuArgAsnArgPheLeuValArgThrAsnGlyAspGluMetGlnValAspGlu 37
; TILE KEFEKRULE: 39-215-3241); CURRENT PAPLICATION NUMBER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14	1162 CGATATAGTCATAGAGTAGAGTTCATACGGTTATATCAGGGTTCCATGCTGCAACC 1
; NUMBER OF SEQ ID NOS: 204966 ; FEQ ID NO 110193	377 LyscysAsnGinCysValGiuGiuMetGinSerTnrAlaAlaArgPheAsnSerWetVal
; LENGTH: 518 ; TYPE: PRT ; ORGANISM: Oryza sativa	OY 1222 GAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAAACCGTTTCC 1269
; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1427C.1.pep US-10-437-963-110193	1270 TTCTTATACAAGAACCTGAGAGAGAATCTGCAAGAAGATAATC
Length:	Db 417 AlaAlaTyrArgArgValArgArgArgValMetGlyGlnLeuValAlaAlaAlaThrAla 436 Oy 1315TCTATGGATCTGTATTGGAGAGGCAAAGACAAGAC
465.00 Matches: sint Similarity: 46.53% Conservat Total Similarity: 20.54% Matches	:::
der March: minimitry: 52.018 indels: 14.168 indels: B: 16.188 daps:	Qy 1360 ACCTCTATGTTCCACCAGCATTGCCTTCTCAGCAGCGAAACGAAAGAACCATCAGATT 1419
US-09-423-575-1 (1-1886) x US-10-437-963-110193 (1-618)	400 OELDOELFHEELEGALLINGSILGENALSILGAARGEGALAGALGALGALGALGALGALGALGALGALTAGALTAGAGALTAGAGALTAGAGALTAGAGALTAGAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGAGATAGAGAGATAGAGATAGAGATAGAGAGATAGAGAGAAGA
Qy 583 CCACTTCATCCTTTGGATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGT 642	476 TrpArgProGlnArgGlyLeuProGluLysSerValAlaValLeuLysAlaTrpMetPhe
643 TITGAAGCAAATAGTGAGTTTCAGGCATTTCAGGTGTAGTTGGTCCAAGTGAACCAATG	Qy 1480 CAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGT 1539 :::
beuselfickieriaalaselsel ACATTCGGTGAAGAAGATTTCCCGTTTCTAATTTCGAATAAAAGAAACAATGAG 	Qy 1540 GGCTIGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGGGGGTTAGGAAG 1599
Db 181 AlaSerGlu 183 Qy 763 CTTTCATTGAGTCTTGCATTCAGATGTTTCTGATGAATGC 801	1600
	536
802 TCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAG 84	
DD 204 SetGiuvalseicysseigiybeunninisvalseisergiygiydiydiydis 223 Qy 844 CAAGCTTCTTGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGT 894	; FUDITIOALION NO. USZUO4UIZ3343AI ; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J.

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Sequence 180416, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yougwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY NUCLEIC Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY NUCLEIC Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: SOY NUCLEIC Acid Molecules Associated With
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TITLE OF INVENTION NUMBER: US Acid Molecules Aci
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| 311 AlaGlyGlnValArgAlaAlaSerArgAlaLeuGlyGluAlaValAspAlaAspGlyGly
                                                                                                    GluAsp---SerGluGlyValSerGlyGlyGlyThrGluAspGlyGlyGlyAlaLysSer
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ORGANISM: Glycine max
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US-10-424-599-180416
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APPLICANT: caou, Yinua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Numbers: US/10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162637
TYPE: T
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|AsnLeuTrpThrProAlaAlaAlaThrGly-----,----AlaGlyAspMetSerPro 108
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|SerArgGluAlaAlaProProValThrValAlaAlaValValAlaAlaGlyAspGluGly 153
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_6170C.1.pep
US-10-437-963-162637
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ORGANISM: Oryza sativa
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QY 1474 ATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATA 1533 Db 313 LeuPheGluHisPheLeuHisPheLeuHisProTyrProSerAspValAspLysHisIleLeuAlaArg 332 QY 1534 CGAAGTGGCTTGACAAGAAGTCAGGTTTATAAATGCGGGTTAGGCTA 1593 Db 333 GITTHTG1YEUSETAGAAGATGGAATGAACTAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	SULT 11 SULT 11 SerGlucysalaSerSerIleIleAsnAsn SULT 11 Sequence 43080, Application US/10425114 Publication No. US2004003488A1 Sequence 43080, Application US/10425114 Publication No. US2004003488A1 APPLICANT: Liu, Jinhua APPLICANT: Liu, Jinhua APPLICANT: Screen, Steven E APPLICANT: Babska, Jack E APPLICANT: Screen, Steven E APPLICANT: Babska, Jack E APPLICANT: Screen, Steven E APPLICANT: Scre	Alignment Scores:
State Similarity: 29.56# Mismatches: 152 13.49# Indels: 88 17 13.49# Indels: 15 17 18.49# Indels: 17 18.49# Indels: 17 17 18.40# 18.4	09 784 GATGTTTCTGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGC 837	09 1174 TGCGTAGATGATATCATACGGTTCCATGCTGCAACCGAGTTAGAT 1230 200 TyrArgAsnGliMetLysSerValvalSerSerPheGlualaValaladlyasnGlyala 219 09 1231 CCACAGTTACACACCCGGTTTGCCTCCAACCGTTTCTTATACAAGAACTGAGA 1290 220 AlaThrValTyrSerAlaLeuAlaLeuLysAlaMetSerArgHisPhargCysLeuLys 239 09 1291 GAGAGAATCTGCAAGAAGAAAACTACTATTCTTCTTTTATACAAGAACTGAGA 1290 240 AspGlylleLeuSerGlnlleGlnAlaThrArgLysAlaMetGlyGluLysAspProVal 259 09 1315 TCTATGGGATCTGTATTGGAGAAGAGCAAGACAAGACT 1353 250 AlaProGlyThrThrArgGlyGluThrProArgLeuLysVallleAspGlnThr 277 09 1354 CAAGAAACTCGCAGCATTGCTTCTCTCAGCAGACGAAACGAAACGAAACCAT 1413 Db 278LeuArgGlnGlnArgAlaPheGlnGlmetSerMetMetGluThr 292 09 1414 CAGATTTGGAGACCTCAACGGGTTTGCCTTCTTCAGCAGTCTACCGAATTGC 1473 Db 293 HisProTrpArgProGlnArgGlnGlnArgAlaPheGlnGlmetSerWetLeuArgAlaTrp 312

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Qy 1279 AAGAACCTGAGAGAGAATCTGCAAGAAGATAATCTCTATGGGATCTGTATTGGAGAGA 1338	ò	652 AATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATGATGTCT 708
98	дG	
Qy 1339 GGCAAAGACAAGACTCAAGAAACCTCTATG	ò	
luGlyserArgi	ਵਰ	HisAsnAsp
Qy 1369TTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAGGAACCATCAGATTTGGAGA 1425	Qy Dp	709 ACATTCGGTGAAGAAGATTTCCGATTATCGAATAAAAGAACAAT 759
1426	<u>ک</u> ک	760GAGCTTTCATTGAGTCTTGCATCAGATGTTTCTGATGAATGC 801
GGCTTG	à	TOGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGC
	qo	160 SerTyrProTyrTrpSerAlaLysThrGluLeuThrProHisSerTyrHisGlyAsp 179
OY 1546 ACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATG 1605	çy qa	862 AAAGACATITCTAATAACGITGTTACTCAAGGITTCTCTCAAATTTTGGCTCAAAA 921 :::
Qy 1606 ATAGAAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGT 1653 Db 204 ValGluGluMetTvrLeudluGluVallvysGlnGluProAsnAsnSer 219	S S	922 TACCTTCACTCTGTTCAGAAATACTATCTCCATTTCGCCGCATACTCGCTCG
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1 2 2 1	qq	:::
; Publication No. US20040123343A1 ; GENERAL INFORMATION:	70	1042 ACTGAGITICITGAIGGIGATICIAAIAACICGGAGGCGGGTTICGGA 1089
	qq	nnysgluðlagluglyglyserLysglyglu
APPLICANI: ZHOU, IIHUA APPLICANI: Go, YOGWei . ADDIICANI: W. Wei	ζ	
; APPLICANT: Barbaruk, Andrey A.: APPLICANT: Barbaruk, Brad	qq	GlyValSerSerAsnProGlnGluSerThrAlaAsnAlaAlaProGluIleSerAlaAla
Li, Ping WENTION: Ri	.; q a	1099 CAAAGGAGAGCAAAGAAAGAAAACCCATCTCTTGGATCTTCTTCAAATGGTGGTGAT 1158
; FILE REFERENCE: 38-21(53221)B ; CURRENT APPLICATION NUMBER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14	& &	1159 GATGGATAGACATTGCGTAGAGATTCATACGGTTATATCAGCGTTCCATGCT 1215
NUMBER OF SEC 1D NOS: 204900 SEC 1D NO 134068 LENGTH: 642	i ò	
; TYPE: PRT ; ORGANISM: Oryza sativa	q _C	
; FEMILYES: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_35878C.1.pep US-10-437-963-134068	AG QG	1276 TACAAGAACCTGAQAGAGAGAATCTGCAAGAAGATAATCTCTATGGGATCTGTATTG 1332
4.77e-34 Length: 439.00 Matches:	8 8	
rcent Similarity: 44.30% Conservative: 6 st Local Similarity: 29.39% Mismatches: 1 sry Match: 13.37% Indels: 1	8 8	
DB: 14 INS-09-423-575-1 (1-1886) x US-10-437-963-134068 (1-642)	qq	dlnLeuArgGlnGlnArgAlaPheGlnGlnTyrGlyLeuLeuGlnGln
532 GTTCAAGATAACCGCAATGTTGAGGCTCCTCCTCCTCTCTCT	ð í	1408 AACCATCAGATTTGGAGACTTCAACGAGGTTTTGCTGAGAAATCTGTTTCGGTTCTACGG 140,
Db 54 IleGlnHisGlnGlnAsnPheMetGluLeuProGlyHisProThrAlaIle 70	g 2	
Qy 592 CCTTTGGATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGTTTTGAAGCA 651	ž	

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NOS: 204966
SEQ ID NO 143490
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       CTICITCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTTATA 1200
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                                                                                                                  SerSerPheAspAlaValAlaGlyAlaGlyAlaAlaArgProTyrThrAlaLeuAlaLeu 161
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                               TCAGCGTTCCATGCTGCAACCGAGTTAGAT --- CCACAGTTACACACCCGGTTTGCCCTC
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182 LeuargargserLeuGlyGluLysAspGlySeralaGlnGlyGlyGlyLeuProArgLeu
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
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ORGANISM: Oryza sativa
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CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 48619
                                                                                                            1588 AGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAAT 1647
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398 AlaTrpLeuPheGluHisPheLeuHisProTyrProLysAspSerGluLysLeuMetLeu 417
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                                    GCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTT
                                                            ||||||| ::: :::|||:::|||
42 TyrLeuLysAlaAlaArgGluLeuLeuAspGluValValAsnValGlnAspAlaIleLys
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US-10-425-114-48619
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ORGANISM: Zea mays
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562	GCTCCTCCTCCTCCTCCTCCACTTCATCCTTTGGATCATTTAAGACACA	8 1
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664	CAGGCATTTTCAGGTGTAGTTGGTCCAAGTGAACCAATGATGTCTACATTCGGTGAAGAA	8
132		a :
724	4 GATTICCCGTITCTAATTICGAATAAAGAACAATGAGCTITTCATTGAGTCTTGCATCA 783	, a
784	GAIGTITCIGAIGAAIGCICGGAGAIAAGICITIGIGCAGCIACAAGAIIAGCC 8	RES US-
157	::; 7 GlnIleMetAlaProSerLeuProTyrTrpSerIleLy8ProAspMetLeuThrProGln 176	
838	8 TCAGAGCAAGCTTCTTGCAGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTC 897	
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197	SerargalaileArgAsnSerArgTyrLeuLysAlaAlaGlnGluLeuLeuAspGluVal	
958	8 GCCGCATACTCGCTCGATATTCATCTCGAGGAACCGAGTCAGGAGCT 1005 ::: 7 ValSerValTrDLvsSerIleLvsGinLvsAlaGlnLvsGluLvsValGluSerClvLvs 236	
1006	6 GOTAGIICAGCCITIACTICACGITITGAGAAIAIAACIGAGIIICIIGAI 1056	••••
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1162	.2 CGATATAGTCATTGCGTAGATGAGATTCATACGGTTATATCAGCGTTCCATGCTGCA 1218 	DB:
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Σ.	1279 AAGAACCTGAGAGAGAATCTGCAAGAAGATAATCTCTATGGGATCTGTATTGGAG 1335	λο

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APPLICANT: Lassa Thomas J
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OTHER INFORMATION: Clone ID: PAT_MRT3847_16404C.1.pep
-10-424-599-193114
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Publication No. US20040031072A1
GENERAL INFORMATION:
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ORGANISM: Glycine max
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1462 CTACGGAATTGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACAT 1521

50 LeuargalatrpWetPheGlnasnPheLeuHisProTyrProLysAspasnGluLysHis 69

25 G G G

30 ArgAsnGluGlnGlnGarTrpArgFroGlnArgGlyLeuProGluLysSerValSerVal 49

1522 CTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCG 1581

70 LeuleuhlaileGinSerGlyLeuThrArgSerGlnValSerAsnTrpPheileAsnAla 89

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Copyright (c) 1993 - 2004 Compugen Ltd.
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This sequence represents the Arabidopsis thaliana ATH1 homeobox gene. The invention relates to a plant gene construct comprising a complete or partial DNA sequence coding for an ATH1 gene product under the control of a promoter functional in plants. The construct can be used to modify (either promote or retard) flowering in plants. The construct can also be used in a method of producing a transgenic plant that lacks the shade avoidance response of a wild type plant
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ACTICACGITITIGAGAATATAAACIGAGITICTIGAIGGIGATICIAATAACICGGAGGCG 108	1081 GGTTTCGGATCTACATTTCAAAGAGAGCATCAGAAACCAAAGAAAACCCATCTCTTGGAT 1140 	1141 CTTCTTCAAATGGTGGATGATCGATATGATCATTGCGTAGATGAGATTCATACGGTTATA 1200 	1201 TCAGGGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCGGGTTTGCCCTCCAA 1260 	1261 ACCGTTTCCTTCTTATACAAGAACCTGAGAGAGAGAGAGA	1321 GGATCTGTATTGGAGGGGAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCAT 1380 	1381 TGCCTTCTTCAGCAGCTGAAACGAAACGAACCATCAGATTTGGAGACCTCAACGAGGTTTG 1440 	1441 CCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCCTTC		TCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTAT 	168	CGAATGCCAAAATCTGTTATGATGAGCCAAGCAATGCATAAATAA	141 TACCAACTTTGTGATAATTAGGCAATTGCTACTCTATGATTGCCCAAACCTAAACCATG 180 	801 TACGACTATCATTACCTATGTTATAATTGT 	1861 ATTTATTAAAAAAAAAAAAA 1886 	ULT 2 11039 ABK11039 standard, DNA, 9359 BP.	ABK11039; 05-JUN-2002 (first entry)	XX DE pVDH636 vector containing Arabidopsis AtH1 gene. XX FW pVDH636 vector; circular; cyclic; grass; plant; herbicide resistance;	<pre>baseball; cricket; football; golf; rugby; soccer; tennis; lawn; park; athletic field; animal feedstuff; grass flowering inhibitor; AtH1; gene; ds.</pre>
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st Local Similarity 99.9%; Pred, No. 0; tches 1884; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	TATAAATGTTGCTATTTGTTG	ATGAGATATGAATTTCTTCATGAATTATTGTAAGAAAAGAACATAGAGAGCT	GCGGAATGAAAGTACACTGTTCTTCACGGAGAAAGAAGAAATAAAT	B1 CTTCAGTTTTTAACACATTTTGAAATTTTGAAAATTCTCTTTGGAACGTGTTGTTCTTTTTTTT	41 GTTGTCTGAAATCTTCCCAAAGGTTCTATCAGAAGAAGAAGAAGATTCATAGAAACA GATTCATAGAAACA GATTCATAGAAACA GATTAAAAAAAAAA		CAAAATCCTCTTCTCATGGATTTTATACCTTCAAGAGAAGATTCAACTTCATTCTCAACA	21 ATGCTTCCATGGAATACCATCAGATCCTCTACAAATGGGTGGCTTTGATATTTTC	AATTCTAIGCTGACTAACAAATACTTATCATCTTCTCCACGGTCTATCGATGTTCAAGAT	541 AACCGCAATGTTGAGTTCATGGCTCCTCCTCATCCTCCTCCTCATCCTTCATCCTTTGGAT 600 [CATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGTTTTGAAGGAAATAGTGAG 	661 TITCAGGCATITICAGGIGTAGTIGGICCAAGTGAACCAATGATGICTACATITGGGTGAA 720 	721 GAAGAITICCCGITICTAAITICGAAIAAAGAAACAAIGAGCITICAITGAGICTIGCA 780 	781 TCAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCA 840 	841 GAGCAAGCTICTIGCAGCAAGACAITICIAAIBACGTIGTIACICAAGGTITCICT 900	901 CAACTIAIAITIGGCICAAAATACCIICCACICIGIICAAGAAATACIAICICAITICGCC 960 	961 GCATACTCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTT 1020 	1021 ACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCG 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a grass plant, which has been genetically modified to substantially inhibit generative propagation and carry herbicide resistance. The grass is useful for growth and/or propagation of grasses. The grass is used to play at least one sport (e.g. baseball, cricket, football, golf, rugby, soccer or tennis), or used at least in a portion of an athletic field, lawn or park. The grass is fed to animal feege, cattle, goat, horse or sheep) or used as an animal feedstuff. The present sequence represents the coding sequence of pVDH636 vector containing the Arabidopsis AtH1 gene, which was used to inhibit flowering in grasses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genetically modified grasses that express inhibited generative propagation, or herbicide resistance, useful for forage (e.g. cattle feedstuff) or amenity purposes (e.g. for use in an athletic field, lawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCAATGGACAACAACAACAACAACAACAACACTTTTAGTTCTCTGGATAATGTCATGACTA
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27-NOV-2000; 2000US-0253274P.
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                                                                                                                                                                                                                                                                           2001WO-EP009572
                           Zea mays.
Agrobacterium tumefaciens
                                                   Oryza sativa.
Escherichia coli.
Cauliflower mosaic virus
Synthetic.
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           Arabidopsis thaliana
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P-PSDB; AAU76514.
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Best Local Similarity
Matches 1476; Conserv
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genetically modified grass is useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), lawns, parks and other types of landscaping. The grass is also useful as an animal feedstuff for cattle, goats, and sheep, due to its increased vegetative growth, improved digestibility blasmid pyth636 but a sanimal feedstuff. This sequence represents plasmid byth636 bu. This plasmid was used as a transformation vector for production of transgenic grasses expressing the Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                       <u>acccaarggacaacaacaacaacaacacacrrrragrrcrcrggaraargrcargacra</u>
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                                                                                                                                                                                                                                                                                                                                                                                                               359 ACCAAAATCCTCTTCTCATGGATTTTATACCTTCAAGAGAAGATTCAACTTCATTCTCAA
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grass; plant, transgenic; flowering inhibition; inflorescence; gene; ds; tiller production; delayed heading; gibberellic acid; phytohormone; golf; genetically modified grass; athletic field; sport; baseball; cricket; football; rugby; soccer; tennis; lawn; landscaping; cattle; horse; sheep; goat; animal feedstuff; Arabidopsis thaliana; AtHI; homeobox gene; circular; cyclic; pVDH636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a grass plant which has been genetically modified to substantially inhibit generative propagation. The genetic modification may result in a heritable change in one or more plant characteristics such as inhibition of flowering (or substantial delay production of tillers, delayed heading and inhibition of the amounts to inhibition), absence of inflorescence, increased developmental switch from vegetative to generative growth. A method of making a grass involves transforming the grass with a nucleic acid which interferes with metabolism of gibberellic acid. A grass can be treated by applying a phytohormone to at least partially relieve or reverse a change in plant characteristic resulting from genetic modification. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genetically modified grass useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), or as animal feedstuff for cattle, goat, horse and sheep.
                                                                                                                 ATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACCAACTC
                                                                                          Smeekens SCM, Proveniers MCG;
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                                                                                                                                                                          TITACCAACTITGIGATAATTAGGCAATTGCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformation vector plasmid pVDH636 DNA.
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27-NOV-2000; 2000US-0253274P.
27-JUN-2000; 2000US-0253327P.
22-JUN-2001; 2001US-0300220P.
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P-PSDB; AAU76885.
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                                                  6245
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1018

1139 ATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTTA

CGGGTTTCGGATCTACATTTCAAAGGAGAGAGCATTAGAAGCAAAGAAAACCCATCTTGG 5705 CGGGTTTCGGATCTACATTTCAAAGGAGGATTAGAAGCAAAGAAAACCCATCTTGG

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TATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCC 5825 TATCAGGGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCGGGTTTGCCCTCC AAACCGTTTCCTTCTTATACAAGAACCTGAGAGAGAGAATCTGCAAGAAGATAATCTCTTA AAACGGTTTCCTTCTTATACAAGAACCTGAGAGAGAGAAAATCTGCAAGAAGAAGAATAATCTCTA TGGGATCTGTATTGGAGAGGCAAAGACAAAGACTCAAGAAACCTCTATGTTCCACCAGC 5945 TGGGATCTGTATTGGAGAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACAGC 1379 ATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTT ATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTT **ACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGG** 6125 ACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGG TATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGT

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0; Gaps Query Match 6.8%; Score 128.4; DB 3; Length 323; Best Local Similarity 67.7%; Pred. No. 9.5e-22; Matches 180; Conservative 0; Mismatches 86; Indels 0;

ö 74 TCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTC 1370

1489 AACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCC 1430

TICACCCTIACCCGAAAGAITCGGAGAACAICTICIAGCIAIACGAAGIGGCTIGACAA 1549 Agadadagactrocreasecerorierriceinterecentesecentesecentesecentere 1490 75

AAGAGATGTATGCGGAAATGAACAAG 1635 AGGAGATGTACATGGAAGAACTCAAG 280 1610

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DNA; 343 AAC56856 standard;

BP.

AAC56856;

Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeodomain; homeocix; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.

Pinus radiata transcription factor DNA sequence #87.

(first entry)

25-JAN-2001

AAC56287;

(first entry) 25-JAN-2001 Pinus radiata transcription factor DNA sequence #302.

Plant, transcription factor; gene expression, eucalyptus, pine, acacia; poplar, sweetgum, teak; mahogany; bZIP, G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain, APZ, EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.

Pinus radiata

WO200053724-A2

14-SEP-2000

GENESIS RES & DEV CORP LTD. FLETCHER CHALLENGE FORESTS LTD.

(GENE-) (FLET-)

99US-00266513 99US-0149485P

11-MAR-1999; 18-AUG-1999;

09-MAR-2000; 2000WO-US006112

WO200053724-A2. Pinus radiata

14-SEP-2000

The present invention relates to novel plant transcription factors from Bucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a manogany species or to mathyptus, pine, acacia, poplar, sweetgum, teak, or manogany species or to madify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, APP2 and RREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide. GAAGTCAGGTATCAAATTGGTTTATAAATGCCAGGGTTAGACTATGGAAGCCCATGGTGG TACGACAACAGCGCGCATTTCACCACTTAGGATTGATGGAGCAGCACCCTTGGCGACCGC Sequence 323 BP; 99 A; 67 C; 80 G; 77 T; 0 U; 0 Other; Σ Glenn Claim 1; Page 153; 747pp; English Shenk MA, Mcgrath A, WPI; 2000-579369/54 15 195 Σ Wood g В ద δ ò В ð ð

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1618 6244 1678

6185 TATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGTT

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TITACCAACTITGIGATAAITAGGCAATTGCTACTC 6400 TITACCAACTITGIGATAATTAGGCAATTGCTACTC 1774

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AAC56287 standard; DNA; 323

AAC56287 RESULT

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ATGCGGAAATGAACAAGAAGCTCAATAACAGTCACATTCAACCCAACGGACCAACTC

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Thu Sep

09-MAR-2000; 2000WO-US006112.

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; Arabidopsis thaliana DNA fragment SEQ ID NO: 23512. promoter; termination sequence; ss. AAC39138 standard; DNA; 2025 17-OCT-2000 (first entry) Arabidopsis thaliana. AAC39138;

imes imeAACGAGGITTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCC 1489 GAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAG 1609 The present invention relates to novel plant transcription factors from Bucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a manogany species or to marking modified gene expression such as a manogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the binding families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MbDS, homeodomain zipper, LIM domain, APP2 and BREBS, zinc finger domains of type 2 CysZHis2, CCAAT box elements and ô TTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAA 1549 95 AGAGAGGACTTCCTGAACGCTCTGTNTCTGTTCGTGCATGGTTGTTTGAGCATTTTC 154 recaccerarceaerrearecaerrasecarararecerarecerasecasecreecerases 215 GAAGTCAGGTATCAAATTGGTTTATAAATGCCAGGGTTAGACTATGGAAGCCCATGGTGG 274 94 New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide. 1370 TCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTC 35 raccacacacaccacarrircaccacriascarricacacacacacacacacacacacac 0 Ouery Match 6.8%; Score 127.4; DB 3; Length 343; Best Local Similarity 67.3%; Pred. No. 1.7e-21; datches 179; Conservative 0; Mismatches 87; Indels 0; Sequence 343 BP; 106 A; 70 C; 86 G; 79 T; 0 U; 2 Other; AAGAGATGTATGCGGAAATGAACAAG 1635 AGGAGATGTACATGGAAGAACTCAAG 300 Claim 1; Page 530; 747pp; English.

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Query Match

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2000EP-00301439 99US-0129845P. 99US-0130077P. 99US-0130510P. 99US-0130891P. 25-FEB-2000; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 23-APR-1999; 23-APR-1999; 28-APR-1999; EP1033405-A2 21-APR-1999; 05-MAY-1 06-MAY-1 06-MAY-1 11-MAY-1 14-MAY-1 14-MAY-1 18-MAY-1 18-MAY-1

99US-0127462P. 99US-0128234P. 99US-0128714P. 99US-0125788P. 99US-0126264P. 99US-0126785P. 99US-0132048P. 99US-0132407P. 99US-0132484P.

Mcgrath A, Shenk MA, Glenn M,

Wood M,

WPI; 2000-579369/54

(GENE-) GENESIS RES & DEV CORP LID. (FLET-) FLETCHER CHALLENGE FORESIS LID.

99US-00266513 99US-0149485P

11-MAR-1999; 18-AUG-1999;

99US-0132485P. 99US-0132486P. 99US-0132487P. 99US-0132863P.

19-MAY-1 20-MAY-1

99US-0136392P.

24-MAY-1 25-MAY-1 27-MAY-1

28-MAY-

990S-0136782P-990S-0137222P-990S-0137528P-990S-013724P-990S-0138094P-990S-0138894P-990S-0138894P-

990S-0139119P. 990S-0139452P. 990S-0139453P. 99US-0139452P. 99US-0139455P. 04-JUN-1 08-JUN-1 08-JUN-1 10-JUN-1 10-JUN-1 14-JUN-1

99US-0139456P. 99US-0139457P. 99US-0139458P. 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1 18-JUN-1

99US-0139462P. 99US-0139463P. 99US-0139750P. 99US-0139459P. 99US-0139460P. 99US-0139763P. 99US-0139461P 8-JUN-1999 18-JUN-1

99US-0139817P. 99US-0139899P. 99US-0140353P. 99US-0140354P. 8-JUN-1999

99US-0140695P. 99US-0140823P. 99US-0140991P. 99US-0141287P.

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990S-0141842P.
990S-0142154P.
990S-0142390P.
990S-0142390P.
990S-0142391P.
990S-0144331P.
990S-014508P.
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AAGAAGTCAGGTATCAAACTGGTTTATAAATGCGGGGGTTAGGCTATGGAAGCCGATGAT GTTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCCAGATTTGGAGACC ; 0 Length 2025 Indels Score 126.2; DB 3; Pred. No. 6.5e-21; 0; Mismatches 83; 99US-0154039P.
99US-0155413P.
99US-0155486P.
99US-0155486P.
99US-0156458P.
99US-0156458P.
99US-015713P.
99US-015731P.
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99US-015931P.
99US-0159331P.
99US-016931P.
99US-016981P.
99US-0160981P.
99US-0160981P. Query Match
Best Local Similarity 68.0%;
Matches 176; Conservative 0 RESULT 7
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AC AAC57132;
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TCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGA 1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or manogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulactory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper,
                                                                      Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeodomain; homeocic, homeocomain; homeocic, homeocomain; zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 CysZHis2; CCAAT box element; MYB; ss.
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68.4%; Pred. No. 1.5e-20;
iive 0; Mismatches 79; Indels 0
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                                    Pinus radiata transcription factor DNA sequence #578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glenn M;
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(FLET-) FLETCHER CHALLENGE FORESIS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 592-593; 747pp; English
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                                                                                                                                                                           MADS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide.
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                                                                                                                                       Plant; transcription factor; gene expression; eucalyptus; pine; poplar; sweetqum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
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                                                                                                       Pinus radiata transcription factor DNA sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FLET-) FLETCHER CHALLENGE FORESTS LTD
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AAC56228 standard; DNA; 462
                                                                     (first entry)
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Matches 171; Conservative
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                                 AAC56228;
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1566 CTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGA 1625

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1266 TAAGCAAACAGGACTCACTCGTAGCCAGGTGTCGAACTGGTTTATAAACGCGAGAGTTCG 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel environmental stress-responsive promoters (ADB23163-ADB23252) from Arabidopsis thaliana. The promoters are useful in constructing and breeding stress-resistant plants for applications in agriculture and horticulture. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1410 CCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTATGGAAGCCGATGAAGAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAA
                                                                                                1326 GTTATGGAAACCAATGGTGGAGGAGGTGTACATGGAGGAAATGAAGGAGCAGGCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructing and agriculture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Environmental stress-responsive promoter-related DNA, SEQ ID 153
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2.9e-20;
74;
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breeding stress-resistant plants for applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; environmental stress; promoter; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%; Score 123.6;
19.4%; Pred. No. 2.9e
.ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 470-475; 520pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujita M;
                                                                                                                                                                                                                                                                                                                                ADB23149 standard; DNA; 2043 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-NOV-2002; 2002WO-JP011955.
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29-JAN-2002; 2002JP-00020329
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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Matches 168; Conserv
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                                                                                                                                                     1650 CA 1651
                                                                                                                                                                                                        CA 1387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rrescrictrical acatricarical actrical actrices and actrical actrica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 144; SEQ ID NO 1337; 577pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 1337,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant; gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                          ABZ13532 standard; DNA; 2043 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                  1626 AATGAACAAG 1635
                                                                                                                                  GGAAACAAAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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The invention relates to a number of isolated Arabidopsis thaliana CDNA sequences and their encoded proteins which are especially transcription factor related CONA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or alteration is a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower sensecence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                              ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
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,, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.6%; Score 123.6; DB 9; Length 2385;
59.4%; Pred. No. 3e-20;
ve 0; Mismatches 74; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Riechmann JL, Adam LJ, Dubell AT
Jiang C, Reuber TL, Creelman RA,
                                                                                                                                                                                                                         Plant yield-related polynucleotide clone G1589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 332; 454pp; English.
                                                                                                                      ADD30303 standard; cDNA; 2385 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
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                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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P-PSDB; ADD30304.
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Pilgrim ML,
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1650
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1384 TIGGCTCTTCGAACACTTTCTTCATCCATACCCTAAGGATTCGGACAAGCACATGCTAGC 1443
                                                                                                                                                  1504 GTTATGGAAACCAATGGTGGAGGAGGATGTACATGGAGGAAATGAAGGAGCAGCAAAGAA 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homostic/homeodomain/homeobox/MRDS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and
                                      TATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAG
                                                                           1444 TAAGCAAACAGGACTCACTCGTAGCCAGGTGTCGAACTGGTTTATAAACGCGAGAGTTTCG
                                                                                                               1590 GCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGAGGAAGCTCAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant, transcription factor; gene expression; eucalyptus; pine; acaci, poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; REBES; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eucalyptus grandis transcription factor DNA sequence #77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FLET-) FLETCHER CHALLENGE FORESTS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 64-65; 747pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-2000; 2000WO-US006112.
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Gaps ·.

6.5%; Score 122.2; DB 3; Length 529; llarity 66.5%; Pred. No. 3.9e-20; Conservative 0; Mismatches 88; Indels 0

Best Local Similarity
Matches 175; Conserv

Query Match

1383 1529

1410 CCATCAGAITTGGAGACCTCAACGAGGITTGCCTGAGAAATCTGTTTCGGTTCTACGGAA 1469

1324 CAATAATGCTTGGAGACCTCAACGTGGTCTCCCAGAACGAGCGGTCTCAGTTCTCCGTGC 1470 TIGGAIGTICCAAAACTICCTICACCCTIACCCGAAAGAITCGGAGAACAICTICTAGC

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Conservative

Similarity

Best Local Sim: Matches 168;

Sequence 529 BP; 152 A; 127 C; 138 G; 112 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                     988 CGTGCTTGGCTCTTTGAGCATTTTCTTCACCCTTACCCAAAGGATTCTGATAAGATCATG
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                                                                                                          1405 AAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAATCTGTTTCGGTTCTA
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  ); DB 6;
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; Score 121.8; E
; Pred. No. 7:3e-
0; Mismatches
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	SD66	9906	9066	9D66	3066	3066 3066	9066	9066	9066	9908	9066	3066 3066	9908	8066 8066	8066	SD 66	9908	8066 8066	SD66	8066 8066	9908	9908	8066	8066	S1166	SD66	9908	SD66	SU66	8066 8008	SU66	SD66	SD66	9908	8066	8066 8066	8066	SD66	SU66	99US	SD66	SD66	9908	99US	8066 8066	9908	S066	
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23-575-1	<u> </u>	주면 당면	PR	9. 0. 8. 0.	9 H	7. A.	24 C	7. P.	K. 6		PR	7. G		. R	자 라	. A.	24 G	자 또	9 t		K 6	PR			74 G	. K	T	K. G.	됐 .		G. 5	7. T.	a l	X, 0	PR I	7 G	G	D, D,	다	주 .	Y. A.	몫 t	보다	P				
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14 - MAY - 1999; 14 - MAY - 1999; 15 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 25 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - M
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                                                                                                                                                                                                                                                                                                                                              GGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGA 1625
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                                                                                                                                                                                                                                     165 CTTCTGTTTTGGTTCTCCGTGCTTGGCTATTTGAGCATTTCCTCCACCTTATCCAAAGG
                                                                                                                                                 1388 TTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGA
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                                                                                Ouery Match 6.4%; Score 121.2; DB 3;
Best Local Similarity 69.3%; Pred. No. 8.1e-20;
Matches 165; Conservative 0; Mismatches 73;
 99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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28-OCT-1999;
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29-OCT-1999;
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27 - JUL - 1999;
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04 - AUG - 1999;
04 - AUG - 1999;
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05-AUG-1999;
06-AUG-1999;
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                                                                                                                                                                                             Gaps
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0
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6.4%; Score 119.8; DB 3; Length
Best Local Similarity 67.3%; Pred. No. 2.2e-19;
Matches 169; Conservative 0; Mismatches 82; Indels
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99US-0161405P.
99US-0161359P.
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Sequence 19, Appl
Sequence 195, Appl
Sequence 14, Appli
Sequence 14, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 1, Appli
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Sequence 11, Appli
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Sequence 101, App
Sequence 927, App
Sequence 2237, Ap
Sequence 2813, Ap
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/cgn2 6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2 6/ptodata/2/ina/6A_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-620-3120-927

US-09-621-976-2317

US-09-621-976-2313

US-09-621-98-61

US-09-621-98-61

US-09-621-98-61

US-09-621-976-594-195

US-09-122-4008-5

US-09-428-034-1

US-09-428-034-1

US-09-621-976-683

US-09-624-945-2

US-09-619-459-1

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US-09-134-000C-2630
US-09-976-594-690
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US-09-716-129-42
US-09-598-401C-23
US-09-621-976-2813
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US-09-358-082A-28
US-08-956-171E-662
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Score Match Length DB
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1886
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39.2
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JS-09-134-001C-217 Sequence 217, Ap	JS-08-655-352-11 Sequence 11, App	US-09-258-016-11 Sequence 11, App	US-09-257-825B-11 Seguence 11, App			Sequence 1, 7	3, 7	Sequence 55,	801-861-3 Seguence 3, Appl	US-08-956-171E-527 Seguence 527, Apr	Sequence 21, A	US-10-204-708-57 Sequence 57, App		JS-08-956-171E-661 Sequence 661, App	JS-09-381-849-4 Seguence 4, Appl	Seguence 6	TS-09-543-6814-0737
4 US-09-1	3 US-08-6	4 US-09-2	4 US-09-2	4 US-09-4	4 US-09-6	4 US-09-7	1 US-08-2	4 US-10-2	4 US-09-8	4 US-08-5	4 US-09-6	4 US-10-2	4 US-08-9	4 US-08-5	3 US-09-3	4 US-10-2	4 118-09-
096	1720	1720	1720	10640	1892	640681	8878	11015	53332	1565	5340	6326	1057	1078	2079	6801	207
2.0	2.0	2.0	2.0	2.0	2.0	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	6
37.2	37	37	37	37	36.8	36.6	36.4	36.4	36.4	36.2	36.2	36.2	36	36	36	36	a r
28	53	30	31	32	33	34	32	36	37	38	39	2 40	41	2 42	43	2 44	ر 4

ALIGNMENTS

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Sequence 1031, Application US/09976594

Barent No. 6673549

GREAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
ITILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT APPLICATION NUMBER: 2001-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
SEQ ID NOS: 1143
SSCFINE NO 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1531 ATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1591 CTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1471 IGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5%; Score 48; DB 4; Length 2905; 52.5%; Pred. No. 0.0056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No. 6673549 480885.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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US-09-489-847-101
Sequence 101, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 52.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
US-09-976-594-1031
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2905
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1499 ACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGG 1558
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                                                                                                                                                                                                                                                                                                                                                   Score 45.2; DB 4; Length 1579;
Pred. No. 0.024;
0; Mismatches 68; Indels 0
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51.0%; Pred. No. 0.028;
iive 0; Mismatches 101; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1559 TATCAAACTGGTTTATAAATGCGCGGGTTAGGCT 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TAIGTAACTGGTTCATCAATGCCCGGCGGCGGCT 343
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.8%;
Matches 86; Conservative
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Best Local Similarity 51.04
Matches 105; Conservative
                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                           , NAME/KEY: CDS
, LOCATION: (117)..(830)
US-09-620-312D-927
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US-09-134-000C-2237/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 ITCTCTTTGGAACGTTGTGTGTTGTCTTGCAAATCTTCCCAAAGGTTCTATCAGAAGAAGA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAAGCATTATCTTCTTCAGTTTTTAACACACACATTTTGGAAATTTTGATGTAAAAA
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Pred. No. 0.0048;
0; Mismatches 74; Indels
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19
             APPLICANT: Rosen et al
ITTLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                         CURRENT FEATURE: EGG/189, 847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: UC/US99/17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1999-07-30

EARLIER FILING DATE: 1999-08-30

EARLIER FILING DATE: 1999-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/095, 486

EARLIER FILING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/095, 454

EARLIER FILING DATE: 1998-08-06

EARLIER FILING DATE: 1998-08-06
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Patent No. 6569662
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PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: ^^^
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Best Local Similarity 55.4%;
Matches 92; Conservative
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Yang, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
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, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-489-847-101
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APPLICANT: Tang, Y.
APPLICANT: Liu, Che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang,
Wang,
Zhou,
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 8
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 RKWSTWRKSRSYASARSAKRCCYSCSWGAMSWKYMWRWRWRWRGWATGAGMKAWRASCMMR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 RKYAĞKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMWKRW 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 WYAKCWTKWKWSWSYMMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWTWAWRYWRYAMWGTYKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 TCCTCATCCTCCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.4%; Score 44.4; DB 4; Length 832;
Best Local Similarity 13.4%; Pred. No. 0.029;
Matches 50; Conservative 168; Mismatches 149; Indels
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Goldano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 19335
SOFTWARR: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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Fatent No. 5670367
GENERAL INFORMATION:
APPLICANT: BORNER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STREET: VA
COUNTRY: USA
COUNTRY: USA
COMPTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       923 ACCTICACTCTGTT 936
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                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1287 GAGAGAGAATCTGCAAGAAGATAATCTCTATGGGATCTGTATTGGAGAGAGGCAAAGA
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OPERATING SYSTEM: PC-DOS/NS-DOS
SOCTYARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-A061-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.2%; Score 42; DB 1; Le
Best Local Similarity 7.5%; Pred. No. 0.36;
Matches 33; Conservative 210; Mismatches 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1707 CCAAGCAATGCATAAATA 1724
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INFORMATION FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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TELEFAX: (703) 683-4109
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us-09-423-575-1.rni

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                                                                                                                                                                                                                                                                           1029 TGGTTGTTCCAGCACCTCTCGCACCCGTACCCCTCGGAGGAGGAGAAACAGCTGGCG
                                                                                                                                                                                                                                                                                                                                                         1089 CAGGACACGGGGCTCACCATCCTGCAAGTCAACAGGGTTCATTAACGCCCGGAGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 ACTGAAAAAAAAAGAAGCTGAAAATCAATTTTCTAAAGCAATTTTATTTGTAAATCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 CACITITIAGITICITCIGGATAATGICATGACTAACCAAAATCCICTTCICATGGATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 TATCAGAAGAAGAAGGATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAA
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                                                                                                                                      Length 1770;
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0.48;
                                                                                                                                                                                      Indels
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         Incyte ID No. 6673549 995887.12
                                                                                                                                                                                      62;
                                                                                                                                         Score 40.8; DB 4;
Pred. No. 0.38;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09122400B
Fatent No. 6245974
General Information:
APPLICANT: Spiker, Steven:
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
FILE REFERENCE: Michalowski and Spiker
CURRENT APPLICATION NUMBER: US/09/122,400B
CURRENT APPLICATION NUMBER: 06/066,118
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
) OTHER INFORMATION: Incyte ID No. 667354

; NAME/KEY: unsure

; LOCATION: 846, 851

; CTHER INFORMATION: a, t, c, g, or other

US-09-976-594-195
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                                                                                                                                                                                                                                                                                                                                                                                                               1591 CTATGGAAGCCGATGATAGA 1610
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US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
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                                                                                                                                         2.2%;
55.7%;
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; ORGANISM: Nicotiana tabacum
US-09-122-400B-5
                                                                                                                                      Query Match
Best Local Similarity 55.74
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%
Query Match
Best Local Similarity 47.0%
Matches 124, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-122-400B-5
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ENGTH: 998
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
                       APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UVEALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT APPLICATION NUMBER: 60/073,189
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR PILING DATE: 1998-01-30
PRIOR PELING DATE: 1998-01-30
PRIOR SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
LENGTH: 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 CCAATGGACAACAACAACAACAACAACACTTTTAGTTCTCTGGATAATGTCATGACTAAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATGATGAAGATTATGAATTTCTTCATGAAATTATTGTAAGAAAAAGAACATAGAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 TAGGTTTAAATTTTTATTTGCATCTTGTTTAATAATTGCAAGTGGTTTAATAATGCTAAT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 referriaalgarraarricgrirgaarrraaraalarrigereargerigrirriare 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AACAATATTTAACAATTGATAGTGGTGGTTTGCATCTAAATCTTTTGTGTTAATACTTAT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GITGICTGAAATCTICCCAAAGGTTCTATCAGAAGAAGAAGGATAAAGTTTCATAGAAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 Tritafirctraritraaricaactriagiaggaacaaaataarcritraritritcarcaar 441
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Pred. No. 0.39;
0; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 195, Application US/09976594 Patent No. 6673549 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAATCCTCTTCTCAT 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.3%;
Matches 167; Conservative
         Jennifer S.
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NAME/KEY: misc_feature
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US-09-976-594-195
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LENGTH: 1770
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1764 AATTGCTACTCTATGATTGCCCAAAACCTAAACCATGTACGACTATCATTACGTATGTA 1823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 683, Application US/09621976
; Sequence 683, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Uboart, S.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; CURRENT FILING DATE: 2000-07-21
; UUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 683
; LENGTH: 535
                                                   Sequence 1, Application US/09428034
Patent No. 6428956
GENERAL INFORMATION:
APPLICANT: Cheng, Kuc-Joan
APPLICANT: Liu, Jin-Hao
APPLICANT: Tsai, Cheng-Fang
APPLICANT: Hau, Yih-Chin
TITLE OF INVENTION: CELLULASE ENZYMES
FILE REFERENCE: 08919/036001
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Piromyces rhizinflata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.77
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (1)...(1128)
US-09-428-034-1
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Best Local Similarity
Matches 89; Conserv
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; LOCATION: 109..534
US-09-621-976-683
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                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1364
                                                                                                                                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 CATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTTGAGTTCATGGCTCCTC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 CTCCTCATCCTCCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATTCCTCAA 628
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1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match: 2.1%; Score 40; DB 1; Ler Best Local Similarity 2.1%; Pred. No. 1.2; Matches 7; Conservative 187; Mismatches 132;
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY FAGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     629 ACAACATGTGGGGTTTTGAAGCAAAT 654
                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7218 base pairs
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STRANDEDNESS: single
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; CLONE: pTZGpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
PAPLICANT: DIEFENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REPERENCE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT PILING DATE: 2003-05-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
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PRIOR PRILING DATE: 2000-06-30
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PRIOR PRILING DATE: 2000-06-30
PRIOR PRILING DATE: 2000-06-30
PRIOR PRILING DATE: 2000-06-30
PRIOR PRILING DATE: 2000-06-30
1472 GGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTA 1531
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                                                              311 GGATGTATAAGCATCGGTTTAAGGCCTACCTTCAGAAGAAGAAGAAGCAAATGCTGTCAG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAT--CTTCCCAAAGGTTCTATCAGAAGAAGAAGGATAAAGTTTCATAGAAACCCAATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GACAACAACAACAACAACACTTTTAGTTCTCTGGATAATGTCATGACTAACCAAAAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATGGAATACCATCAGATCCTCTACAAATGGGTGGCTTTGATATTTCAATTCT 486
                                                                                                                                    1532 TACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCG 1583
                                                                                                                                                                                                      371 AGAAGACCAATTTGTCTTTGTTGCGGATTTCTAACTGGTTTATCAATGCTCG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; Score 38.6; DB 4; Length 6113; 46.8%; Pred. No. 2.7; ive 0; Mismatches 174; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3337 ATTATTTTAACAATAAATAAATAACCTC 3307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.8'
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249
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RESULT 14 US-09-624-945-2 ; Sequence 2, Application US/09624945

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133 ACCCTTACCCCAGTGAGGAAGCCAAAGAGGAGTTAGCCAAGAAGAGTGTGGCATCACAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1193 cccaddrancaaacrddringdaaaraaccaanccddracaadaagaacar 1244
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Mancewicz, Edward
TITLE OF INVENTION: Antiense Modulation of E2A-Pbx1 Expression
FITLE OF INVENTION: Antiense Modulation of E2A-Pbx1 Expression
FITLE OF INVENTION: UMBER: US/09/624,945
CUREBY APPLICATION NUMBER: US/09/624,945
FRIOR FILING DATE: 1999-09-30
FRIOR PILING DATE: 1999-09-30
SOFTWARE: PATENTIN WERE: 00.156,836
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 2049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

2 0%; Score 38.4; DB 3; Length 2.
Best Local Similarity 49.0%; Pred. No. 1.9;
Matches 102; Conservative 0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.4; DE
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09419459;
Sequence 1, Application US/09419459;
Parent No. 622208
GENERAL INFORMATION:
APPLICANT: Liu, Jin-Hao
APPLICANT: Cheng, Kuo-Joan
APPLICANT: Cheng, Chia-Chieh
ITILE OF INVENTION: CELULASE ENZYMES
FILE REFERENCE: 08919/037001
CURRENT APPLICATION NUMBER: US/09/419,459;
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 10
SEQ ID NO :
LENGTH: 210
TWODE: NA : 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Piromyces rhizinflata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%;
Best Local Similarity 58.9%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (3)...(1749)
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1882 TTTTATTAAAAATAATAAGAAATAAAAA 1855

Search completed: September 2, 2004, 08:25:14 Job time : 144 secs inis Page Blank (uspto)

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Sequence 50272, A Sequence 7110, Ap Sequence 130628, Sequence 110628, A Sequence 11822, A Sequence 5047, Ap Sequence 1337, Ap Sequence 1337, Ap Sequence 1337, Ap Sequence 335, Ap Sequence 2315, Ap Sequence 2315, Ap Sequence 2315, Ap Sequence 2315, Ap Sequence 2315, Ap Sequence 2315, Ap
                                                                                                                                     September 2, 2004, 08:22:57; Search time 887 Seconds (without alignments) 10568.913 Million cell updates/sec
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                                                                                                                                                                                                                            | Can2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Can2 6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Can2 6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Can2 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Can2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Can2 6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| Can2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-114-13353
US-10-437-963-7710
US-10-437-963-7710
US-10-437-963-7120
VS-10-021-323-14220
VS-10-021-323-14220
VS-10-021-323-14220
VS-10-021-323-14220
VS-10-025-114-9882
VS-10-425-114-9882
VS-10-425-114-7804
VS-10-437-963-19673
US-10-938-842A-1337
US-09-938-842A-1337
US-09-938-842A-1337
US-10-225-066A-335
G US-10-374-780A-2671
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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09-922-293-200	9-938-842A-215	39-938-842A-215	10-425-114-1334	10-424-599-1335	10-437-963-6015	10-425-114-2097	10-437-963-4100	10-424-599-1	10-424-599-6387	9-938-842A-905	39-938-842A-90	10-412-699B-63	10-225-066A-8	10-286-264-17	10-374-780A-248	10-424-599-2158	10-425-114-133	10-424-599-6590	6	10-225-068-235	10-374-780A-23	10-437-963-370	10-425-114-7712	10-425-114-29785	10-424-599-37574	10-437-963-50722	10-425-114-1929	10-425-114-2283	10-425-114-3495	10-424-599-5528
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ALIGNMENTS

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Sequence 50272, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)8
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 50272
LENGTH: 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1337 GAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTTCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 GAGAAAAAGATAGAACCTTTGAAACATCGTTTATCAGAGAACAATGGGCTTTGCAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1397 TGAAACGAAAGCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%; Score 171.6; DB 13; Length 422; 72.5%; Pred. No. 8.2e-34; Live 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT3847_16404C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 72.5
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; US-10-424-599-50272
US-10-424-599-50272
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APPLICANT: LI, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 7710
SEQ ID NO 7710
LENGTH: 1995
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF LAST (52233) B
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130628
LENGTH: 3033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AAGGAGCGGAGCTGGGAGTCGTTCATCCAGAAGCACTGGGGCGATGCAGCAGCTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CGCCTCCGACTGTGGAAGCCGATGATCGAGGACATGTACGAGGAGGAGGAGGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130.2; DB 17; Length 1995;
Pred. No. 1.2e-22;
0; Mismatches 103; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 3033;
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US-10-424-599-130628
                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1427C.1
US-10-437-963-7710
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Best Local Similarity 67.5%; Pred. No. 1.6e-22;
Matches 183; Conservative 0; Mismatches 88
                                          Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.1%;
Matches 192; Conservative
Yongwei
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Glycine max
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APPLICANT: Soreen, Yihua
APPLICANT: Soreen, Serven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13353
LENGTH: 15-5-
LENGTH: 15-5-
LENGTH: 15-5-
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                                                                                                                                                 ATGCGCGCGGTTAGGCTATGGAAGCCGATGATAGAAGAGAGATGTATGCGGAAATGAACAAGA 1636
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                                                                                                                                                                              ATGCGAGAGTTCGCCTCTGGAAACCATTGATAGAGGAAATGTACTCGGAGGTAAACAAAA 324
CGGTTCTACGTGCATGGATGTTCCAAAACTTTCTTCACCCGTACCCAAAAGACAACGAAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1370 TCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1430 AACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCC
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6.9%; Score 130.2; DB 13; Length 1555;
Best Local Similarity 67.5%; Pred. No. 1e-22;
Matches 183; Conservative 0; Mismatches 88: Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: JC-GMST02400042B10_FLI
US-10-425-114-13353
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                  1637 GGAAGC 1642
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Best Local Similarity
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US-10-428-114-9882

Sequence 9882, Application US/10425114

Publication No. US20040034888A1

Sequence 9882, Application US/10425114

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 9882

LENGTH: 1716
Sequence 14220, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Raren L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR PAPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
LENGTH: 592
LENGTH: 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COCATION: (1)..(592)
CTHER INFORMATION: unsure at all n locations
CTHER INFORMATION: Clone ID: LIB3829-031-Q6-K6-E4
US-10-021-323-14220
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Gossypium hirsutum
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ORGANISM: Glycine max
FEATURE:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Muses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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       1374 TCAGGCAACAAAGGGCACTTCAGCAGCTAGGAATGATTCAACCCAATGCATGGAGGCCCC 1433
                                                                                                                                                                                        CCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGT 1554
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                                                                                                                                                TTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAA
                                                                                                  1434 AAAGAGGCTTGCCTGAACGAGCTGTTTCCATTCTTCGGGCTTGGCTTTTTGAGCATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1375 CAGCATTGCCTTCTTCAGCAGCTGAAACGAAACCATCAGATTTGGAGACCTCAACGA
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Pred. No. 1.5e-21;
0; Mismatches 81;
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OTHER INFORMATION: Clone ID: PAT_MRT4530_35878C.1
US-10-437-963-31585
                                                                                                                                                                                                                                                                                                                                           1610 AAGAGATGTATGCGGAAATGAACAAGAGGAA 1640
                                                                                                                                                                                                                                                                                                                                                                                         1614 AAGAAATGTACTTGGAAGAAATCAAGGAGCA 1644
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US-10-437-963-31585

Sequence 31585, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Buùkharov, Andrey A.

APPLICANT: Barbank, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1615 ATGTATGCGGAAATGA 1630
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Best Local Similarity 68.4%;
Matches 175; Conservative (
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US-10-021-323-14220
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LENGTH: 2799
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Matches 182; Conservative
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LENGTH: 1785
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                           1430 AACGAGGTTTGCCTGAGAAATCTGTTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCC 1489
                                                                                                                                                                                                                                                                                                                                                   1490 ITCACCCTTACCCGAAAGATTCGGAQAAACATCTTCTAGCTATACGAAGTGGCTTGACAA 1549
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                                                                                                                                                                                                             213 TTCGGCAACAAAGGGCACTTCAGCAACTAGGAATGATTCAGCCCAATGCATGGAGGCCCC 272
                                                                                                                                                                                                                                                                                                     273 AGAGAGCTTGCCTGAACGAGCTGTTTCCATTCTTCGGCCTTGGCTTTTTGAGCATTTCC 332
                                                                                                                                                                                                                                                                                                                                                                                               316 AGCAAAACGCTTGGAGGCCACAGAGAGGACTACCTGAAAATTCAGTCTCGATTCTCGGG 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 GGAGCCAGGTGTCAAACTGGTTTATCAATGCCCGAGTTCGGCTTTGGAAGCCAATGGTTG 452
                                                                                                                                                                 1370 TCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGAGCCTC
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                                                                      Length 1716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGA 1630
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                                                                      DB 13;
                                                                    Score 125.2; DB 1
Pred. No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124.4; DB 1
Pred. No. 3.1e-21;
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                                                                                                                     0; Mismatches
; OTHER INFORMATION: Clone ID: 700875318_FLI
US-10-425-114-9882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: 700441126_FLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 AAGAAATGTACTTGGAAGAAATCAAG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5047, Application US/10425114
Publication No. US/20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                    Query Match
Best Local Similarity 66.9%;
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.5%;
Matches 161; Conservative
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ORGANISM: Zea mays
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Pini
APPLICANT: Li, Pini
APPLICANT: Li, Pini
APPLICANTON: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
Sequence 7804, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Sorien, Steven E

APPLICANT: Sorien, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Sorien, Steven E

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0; Mismatches 96
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US-10-425-114-7804
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Publication No. US20040123343A1
GENERAL INCRMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: BoukEnzov, Andrey A.
APPLICANT: BoukEnzov, Andrey A.
APPLICANT: BaukEnzov, Andrey A.
APPLICANT: BaukEnzov, Andrey A.
APPLICANT: Li, Ping
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Sequence 1337, Application US/09938842A
; Sequence 1337, Application US/09938842A
; Fublication No. US20040009476A9
; Fublication No. US20040009476A9
; GENERAL INPORMATION:
    APPLICANT: Harper, Jeff
    APPLICANT: Wang, Xun
    FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US 60/227,866
; PRIOR PAPLICATION NUMBER: US 60/227,866
; PRIOR PELING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-03-16
; SQ ID NO 337
    LENTH: 2043
                                                 1326 GTTATGGAAACCAATGGTGGAGGAGATGTACATGGAGGAATGAAGGAGGAGGAGGAAGAA 1385
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  1590 GCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAA
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6.6%; Score 123.6; DB 11; Length 2043;
Best Local Similarity 69.4%; Pred. No. 6.3e-21;
Matches 168; Conservative 0; Mismatches 74; Indels 0;
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US-10-225-066A-335
US-10-225-066A-335
Squence 335, Application US/10225066A
PUDLICATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver,
APPLICANT: RECHMANN, JOSE Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBELL, ARIOId T
APPLICANT: PUBELL, ARIOId T
APPLICANT: PICRIM, Marsha L
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ORGANISM: Arabidopsis thaliana
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US-09-938-842A-1337
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Sequence 1337, Application US/09938842A

Sequence 1337, Application US/09938842A

Sequence 1337, Application US/0993842A

Sequence 1337, Application US/0993842A

Patent No. US20020160378A1

APPLICANT: Wreps, Joel

APPLICANT: Wreps, Joel

APPLICANT: Wreps, Joel

APPLICANT: ALW. TORE

TITLE OF INVENTION: SARE, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SARE, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

CURRENT FILING DATE: 2000-08-24

FRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PLING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NOS: 5379
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Best Local Similarity 69.4%; Pred. No. 6.3e-21;
Matches 168; Conservative 0; Mismatches 74;
                                                                                                                                  Query Match 6.6%; Score 124.2; DB 17; Best Local Similarity 65.1%; Pred. No. 4.1e-21; Matches 183; Conservative 0; Mismatches 98;
                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2510C.1
US-10-437-963-19673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1337
ORGANISM: Oryza sativa
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US-09-938-842A-1337
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APPLICANT: Conner, Timothy W.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Transcription in Plants
FILE REFERENCE: 16517.254
CURRENT APPLICATION NUMBER: US 09/922,293
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR PAPLICATION NUMBER: 09/837,944
PRIOR PLING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PLICATION NUMBER: 09/934,455
PRIOR PLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR PLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR PLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
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Pred. No. 7e-21;
0; Mismatches 74; Indels 0;
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Publication No. US20040123339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 69.45
Matches 168; Conservative
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US-10-374-780A-2671
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US-09-922-293-2000
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                                                                                                                 APPLICANT: TINEDA, Omaira
APPLICANT: VU Guo-Liang
APPLICANT: VU Guo-Liang
APPLICANT: VU Guo-Liang
APPLICANT: VU Guo-Liang
APPLICANT: VI Guo-Liang
TITLE OF INVENTION: Yield-Related Polymucleotides and Polypeptides in Plants
TITLE REPERENCE: MBI0036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/316,049
PRIOR PLING DATE: 2001-12-08-09
PRIOR FILING DATE: 2001-12-08-09
PRIOR FILING DATE: 2001-12-08-09
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APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, T. Lynne
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Pineda, Omaira
                                                          REUBER, T. Lynne
CREELMAN, Robert A
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| PRIOR APPLICATION NUMBER: US 09/229,413
| PRIOR FILING DATE: 1999-01-12
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| SEQ ID NO 2000
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| TYPE: DNA | TYPE: DNA | ORGANISM: Glycine max | US-09-922-293-2000
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	Copyright (G) C - protein search, us; September 2, 20 September 2, 20 Core: 3284 1 US-09-423-575-1 CORE: 3284 1 attragtataaaaa able: BLOSUNG2 Xgapop 10.0, Xg Xgapop 10.0, Xg Xgapop 10.0, Xg Ygapop 1	nCore version 1993 - 2004	rame_plus_nzp_model , 11:47:43 , Search time 38 (without alignments 9548.275 Million ce	ttaaaaaaaaaaaaaaaa 188 0.5 7.0 7.0	Chosen parameters: 566732 Chosen parameters: 566732 00 15 summaries	OP 3t	bescription homeobox protein probable homeodom hypotherical protein - BET1-like homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom probable homeodom

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1563
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                   ysHisLeuLeuAlaIleArgSerGlyLeuThrArgSerGlnValSer
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Db 447 MetValGluGluMetTyrMetGluGluMetLysGluGluAlaLysAsnMetGlySerMet 466 Qy 1663 CCCAACGGACCA	F96784 hypothetical protein F1B16.6 [imported] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress) C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C,Accession: F96784 R,Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonn Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 Nature 408, 816-820, 2000	Afauncia: muner, o.i., Jenania: J.; Johnson, A.; Adar, S.; Marcial, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marzial, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Liu, Z.A.; Luros, J.S.; Matti, R.; Marzial, A, Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; WUID: 21016719; PMID: 11130712 A; Recassion: F96784 A; Status: preliminary A; Molecule type: DNA		ty: 42.55% arity: 29.26% 13.52% 2 (1-1886) x F96784 (1-55	Db 22 ABIGINGINGINGINGINGINGINALARASETSETSETSTATABLASETPHESETGI 41 Oy 346ANGTCATGACTAACCAAAATCCTCTCTCATGGATTTATACCTTC 39 A1 ulleValSerGlyAspValArgAsnAsnGluMetValPhelleProPr 57 Oy 393 AAGGAAGATTCAACTTCATCCAACGATCCATGGAATACCATCGATCG	Db 57 othrserAspValAlavalAsnGlyAsnValThrValSerSerAsnAs 73 Qy 453 TCTACAAATGGGTGGCTTTGATATTTCAATTCTATGCTGACTAACAAAACTT 506	Qy 567 TCCTCCTCCATCCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATGATTCCTC 626 Db 101
	814 CTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCAGCAAGAAGACATTCT 873 177	199 AladindiuleuLeuLeuspoluvalvalAsnAlaAspSerAsp	1093	1186 ATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACCC 1242 :::	AAGAAGATAATCTCTATGGAGATCTGTATTGGAGAGAAGGCAAAGACAGAAGACC 13	CTTCAGCAG	407 HisPheleuHisProTyrProLysAspSerAspLysHisMetLeuAlaLysGlnThrGly 426 1543 TTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGGGGTTAGGGTATGGAAGCGG 1602 1543 TTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGGGGTTAGGCTATGGAAGCGG 1602 1603 ATGATAGAAGAGTGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAA 1662 1603 ATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAA 1662

Best Local Similarity: 26.32% Mismatches: 168 Query Match: 12.83% Indels: 190 DB: 2 Gaps: 26.	US-09-423-575-1 (1-1886) x D85435 (1-638)	Qy 289 TITCATAGAAACCCAATGGACAAC315	Db 17 PheHisAsnAsnSerMetSerGlnAspTyrHisHisHisHisHisAsnGlnHisGln 36	Qy 316AALGAGAAGAACACTTTTAGTTCTCTGGATAATGTCATGACT 357	Qy 358 AACCAAAATCCT381	Db 57 GlnGlnLysGlnGluHisGlnArgValGluMetAspGluGluSerSerValAlaGlyGly 76	Qy 382 TITATACCTICAAGAAGATICAACTICATICTCAACAATGCTICCATGGAATACCATC 441	442 AGATCAGATCTCTACAAATGGGTGGCTTTGATATTCAATTCTATGCTG 94ProglySerSerGlyClyGlyGlyGlyGlyGlockSpleuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	QY 493 ACTAACAAATACTTATCATCTTCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTT 552 DD 111 SerAsnArgGlnLeuLeuGlu	Qy 553 GAGTTCATG	Oy 562GCTCCTCCTCCTCCTCCACCTCCA	Oy 586	Qy 613 TATGATGATTCCTCAAACAAGATG	Qy 637TGGGGTTTTGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGT 687	688 CCAAGTGAACCAATGATGTCTACATTCGGTGAAGAAGATTTCCCGTTTCTAATTTCGAAT 	CY 748 AAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGTGTTTCT 792	Oy 793 GATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCA 840	Qy 841GAGCAAGCTTCTTGCAGCAAAAAACATTTCTAATAACGTTGTTACT 888 :: :: :: ::		255 diministration est de la composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della c
¹ 228SerThrileGluargGluGluLeuGlnasnLysLysAsnLysLeuLeuThrMetVala 247 1148 AAATGGTGGATGATGGATATAGTCATTGCGTAGATGAGATTCATACGGTTATATGTGAGGT 1207	247 spGluValAspLysArgTyrAsnGlnTyrTyrHisGlnMetGluAlaLeuAlaSerSerP 267		267 heGluileValAlaGlyLeuGlySerAlaLysProTyrThrSerValAlaLeuAsnArgi 287	1265 TTTCCTTCTTATACAAGAACCTGAGAGAGAAATCTGGAAGAAAAAAAATCTCTATGG 1321 	1322 GATUTGTATTGGAGAGGCAAAGACAAGACTCAAGAAACCTCT 1365	307 lulysLeuGlyGluLysGlyGlyGlyGluSerLeuAspGluGlnGlyGluArglleProA 327	1366	GAAAGAACCATCAGATTGGAGAACTCAGCGAGGTTTGGCTGAGAAATCTGTTTGGGTC etValArgProAlaTrpArgProGlnArgGlyLeuProGluAsnSerValSerValL	1463 TACGGAATTGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATC 1522 	1523 TICTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGC 1582 	1583 GGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGA 1630 	1631 ACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACCAACTCTTCGAATGCCAA 1690	1691 AATCTGTTATGATGAGCGAAGCAATGCATAATAAGAGAACAACAATTGTGTTTACCAACTTT 1750	1751 GTGAT 1755 466 laAsp 467	E E	16-Feb-2001 onsortium, The Cold	of, 789-77, 1999 Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. In passass	: printingiy le type: DNA es: 1-638 <sto> references: GB:NC_001268; NID:g7270636; PIDN:CAB80353.1; GSPDB:GN00140</sto>	28: MT4g36870 sition: 4	Alignment Scores: 2,61e-25 Length: 638

>- O	973 GATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCTTTACTTCACGTTTT 1032	A;Cross-refe C;Genetics: A;Gene: At2g A;Map positi	Cross-references: GB:AE002093; NID:g4544389; PIDN:AAD22299.1; GSPDB:GN00139 Sene: At2g16400 4ap position: 2
	1033 GAGAATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGA 1089	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	<pre>ment Scores: 3.92e-25 Length:</pre>
>-	1135 TTGGATCTTCTTCAAATGGTGGATGATGGTGATTGCGTAGATGAGATTCATACG 1194	0S-09-4	-423-575-1 (1-1886) x HB4539 (1-482)
٩	388 LeuThrMetLeuGluGluValAspArgArgTyrAsnHisTyrCysGluGlnMet 407	δλ	tggggttttgaagcaaatagtgagtttcaggcattttcaggt :::
> 1	GTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACGTTA	ପ୍ପ	7 AspSerThrAsnAsnValSerProSerLysGlulleGlnValLeuSerSer
~ ۵	408 ValValasnSerPheaspileValMetGlyHisGlyAlaalaLeuPro 423 1240 CACACCCGGTTTGCCCTCCAAACGGTTTCCTTATACAAGAACCTGAGAGAGA	& 8	679 GTAGTTGGTCCAAGTGAACCAATGATGTCTACATTGGTGAAGAA 723 :::
۵		δλ	E
ם א	1300 TGCAAGAAGATA	음 상	TAT
>-	1318 ATGGGATCTGTATTGGAGAGGGAAAGACAAGACTCAAGAACCTCTATGTTCCACCAG 1377	qq	88 LeuSerSerGinileGlu 93
۵		δλ	835 GCCTCAGAGCAACTTCTTGCAGCAGAAAAAAAAAAAAAA
>-	1378 CATTGCCTTCTTCAGCAGCTGAAAGAACCATCAGATT 1419	ପ୍ର	nAsnGluTyrAlaThrGln l
۵	LeuleugluginserLeuArgginAsnArgAlaPheHisGinMetGlyMetGlu 494	λ 1	883 GTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTCTGTTCAAGAA 942
s .0	1420TGGAGACCTCAACGAGGTTTGCCTGAGAATCTGTTCGGTTTTGGGAAT 1470 495 GlnGlublaTTpArgFroGlnArgGlyLeuroGluArgSerValAsnIleLeuArgAla 514	8 &	TICGATTATTCATCTCGAGGAACCGAGTCAGGA 10
>-	1471 TGGATGTTCCAAAACTTCCTTCACCCTAACCCGAAAGATTCGGAGAACATCTTCTAGCT 1530	ପ୍ର	::: 127 LeuLeuAspGluThrValAsnValLys135
Ω	w	λŏ	3 GCTGCTAGTTCAGCCTTTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGAT 10
> 0	1531 ATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGG 1590 ::::::	음 상	136 LysalaLeuLysGlnPheGlnProGluGlyAspLysIleAsnGluValLysGluLysAsn 155 1063 TCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGAGAGA
> -	1591 CTATGGAAGCCGATGATAGAAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAAC 1650	qa	
۵	555 LeuTrpLysProMetValGluGluMetTyrGlnGlnGluSerLysGluArgGluArgGlu 574	ò	TCTTCAAAIGGIGGAIGAICGATAIAGICAIIGCGIAGAI 1
>-	1651 AGTCACATTCAACCCAAC 1668	qq	5 LeuSerLysLeuLeuSerIleLeuAspGluValAspArgAsnTyrLysGlnTyrTyrHis 194
b ESULT 6	575 GluGluLeuGluAsn 580	장 음	1183 GAGATTCATAGGGTTATTCATGCTGCAACGGAGTTAGAICCACAGTTA 1239 1181 GAGATTCATAGGTTCCATGCTGCAACGGAGTTAGAICCACAGTTA 1239 1182 GAGATTCATAGGTTCATGGTTCCATGCTGCAACGGAGTTAGAICCACAGTTA 1239 1183 GAGATTCATAGGTTCATGGTTCATGGTAGATAGAICCACAGTTA 1239 1183 GAGATTCATGGTTCATGGTTCATGGTAGATAGAICCACAGTTA 1239 1184 GAGATTCATGGTTCATGGTTCATGGTAGATAGATTAGAT
84539 robable	4539 obable homeodomain transcription factor [imported] - Arabidopsis thaliana Species: Arabidopsis thaliana (mouse-ear cress)	ò	0 CACACCGGTTTGCCCTCCAAACCGTTTCCTTATACAAGAACCTGAGAGAGA
Date: 02-F	02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	අු	SerArgHisPheArgCysLeuArgAspAlaIle 234
Lin, X , Koo, uss, D.		ò d	1300 TGCAAGAAGATAATCTCT 1317 ::: ::: 235 SerGlyGlnIleLeuVallleArgLy8SerLeuGlyGlyGluGlnAspGlySerAspGly 254
ature 4 ;Title: ;Refere ;Access	TRUIRE 402, 761-768, 1999 Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. Reference number: A84420; WUID:20083487; PMID:10617197 Accession: H84539	yy da	1318 ATGGCATCTGTATTGGAGAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAG 1377
;Status ;Molecu ;Residu	Status: preliminary Molecule type: DNA Residues: 1-482 <sto></sto>	ò	1378 CATTGCCTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGT 1437

Db 272 GlnArgAlaLeuGlnArgLeuGlyValMetGlnPrOHisThrTrpArgProGlnArgGly 291 Qy 1438 TTGCCTGAGAAATCTGTTCGGTTCTACGGAATTGGAIGTTCCAAAACTTCACCCT 1497	CY 1174 TGCGTAGATGAGATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGAT 1230 Db 153 TvxHisAsodInmetclnThr11eT1eSerPhedinGlaaladlv.englvser 172
:::	1231 CCACAGTIACACACCCGGTTTGCCCTCCAAACCGTTTCCTTTTTATACAAGAACCTGAGA 12
1498 TACCCGAAAGATTCGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCGG	Db 173 AlaAsnSerTyrThrHisMetAlaLeuGlnThrIleSerLysGlnPheArgAlaValLys 192
312 TyrProLysAspSerAspLysIleMetLeuAlaArgGlnThrGlyLeuSerArgGlyGln 3	1291 GAGAGAATCTGCAAGAAAGATAATCTCTATGGGATCTGTATTGGAGA :::
OY 1558 GTATCAAACTGGTTTATAAATGGGGGTTAGGGTATGGAAGGCGATGATAGAAGAGTG 1617 Db 332 ValSetAshTrpPhelleAshAlaArgValArgUeuTrpLySPrometValGluGluMet 351	Db 193 AspMetIleSerLeuGlnIleLysGlnIleAsnLysLeuLeuGlyGlnLysGlu 210 Ov 1351 ACTCAAGAAACC
1626	211 PheAspGluGlnLeuLysLysLeuGlyLysMetAlaHisHisHis
Db 352 TyrLysdlu 354 RESULT 7	Qy 1396 CTGAAACGAAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTT 1455
C84670 probable homeodomain transcription factor [imported] - Arabidopsis thaliana C. Sharies, Brabidonsis thalians (mouse of all and	1456
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84670	Db 241 SerValLeuArgSerTrpLeuPheGluHisPheLeuHisProTyrProArgAspLeuAsp 260
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 40, 761-768	Qy 1516 AAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATA 1575
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197	Oy 1576 AATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGATGTATGCGGAA 1626
A;Sucus: preliminary A;Molecule 'type: DNA A;Residues: 1-431 <sto> A;Cross-references: GB:AE002093; NID:g6598540; PIDN:AAF18625.1; GSPDB:GN00139</sto>	Qy 1627 ATGAACAAGAGGTCAATAACAGTCACATTCAACCCAACGGACCAACTCTTCGAATG 1686 1::::::::::::::::::::::::::::::::::
C.Genetics: A.Genetics: A.Map position: 2	1687 CCA 1689
Aliqument Scores:	Db 321 Pro 321
Pred. No.: 5.04e-25 Length: 431 Score: 417.50 Matches: 102 Percent Similarity: 50.83\$ Conservative: 51 Best Local Similarity: 33.89\$ Mismatches: 91 Query Match: 12.71\$ Indels: 57 DB: 2 Gaps: 9	RESULT 8 T05281 probable homeobox protein T4L20.190 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 2.3Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C;Accession: T05281
TCTCT 900	submitted to the Protein Sequence Database, September 1998 A,Reference number: 215406 A,Accession: T05281
901 CAACTTATATTTGGCTCAAAATACCTTCATCAAGAAATACTA 948	A;Molecule type: DNA A;Residues: Jac AEEV> A;Cross-reference: EMBL:AL023094 A;Experimental source: cultivar Columbia; BAC clone T4L20
949TCTCATTTCGCCGCATACTCGCTCGATTATTCTCGAGGAACC 993	C;Genetios: A;Map position: 4 A;Introns: 217/3; 340/2; 360/3 A;Note: T4L20.190
DD 95 ASNVALGIYASNGIYSERHISGIYALALYSGINGIUARGPTOVAlSERIYSGIUSERTHr 114 OY 994 GAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCAGGAATATAACTGAGTTTCTT 1053	5.24e-25 Length:
	SOOZE: 134 Percent Similarity: 44.524 Best Local Similarity: 30.598 Mismatches: 159
122	12.71* Indels: 2 Gaps: 1-1886) x T05281 (1-532)
OY 1114 GAAGCAAAGRAAACCCATCTCTTGAATGGTGGATGATATGGTCATATAGTCAT 1173 ::: Db 133 GlnMetLysLysAlaLysLeulleSerMetGlyGluMetValGluGlnArgTyrLysGln 152	481 AATTCTATGCTGACTAACAAAT ::: ::: 13 AspSerWetIleGlnAshalaI
	ro Asparmectrectinamaratievataeriyiserdikaruserhiadiy

ò	541 AACCGCAAHGIIGAGIICAIGGCICCICCICCICCICCACCIICAICCIIIGGAI 600	Š	1521
3 1		q	348
Q O	7	ò	1581
ζζ	CATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGGTTTTGAAGCAAATAGTGAG	QQ	368
qq	4	'n	1627
δλ		q	388
Db	48 LeuSerArgPheGlydlyvalproGlnMetGlnAsnIleGlyGln 62	RESULT	, o
δλ	721 GAAGATTTCCGTTTCTAATTTCG 744	A57632 homeotic	ic prote
Dp	63 AspPheGlySerTrpArgAspGlnAlaSerAspArgAsnGlyPheGlnLeuMetSerAla 82	C;Speci C;Date	ies: Ara
ογ	745 AATAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA	C, Acces	ssion: P
QQ	83 MetalaGlyalaThrGlyIleLeuGlnThrGlyGlnGlyLeuSerLeuSerLeuGlySer 102	Cell 83	3, 735-7
ò	784 GATGITICIGAIGAATGCTCGGAGAIAAGICTITGIGCAGCTACAAGATIAGCCTCAGAG 843	A; Refe	rence nu
qu	103 GlnileLeuProGlylleHisGlnIleSerHisGlnAsnMetAlaProArgGlyAsnGlu 122	A;Stati A;Molec	is: pre
ò	844 CAAGCTICTIGCAGCAGCAAAGACAITICIAAAAAGCIIGTIACTCAAGGITICTCTCAA 903	A, Resid	dues: 1- s-refere
qq	GlnSerPheProGlyGlyAsnGlnA	C, Genet	tics: : BEL1
ò	904 CITATATITGGCTCAAAATACCITCACICTGTTCAAGAAATACTATCTCATITCGCCGCA 963	C, Superfamily: C, Keywords: DN	rfamily: ords: DN
qq	ıLysAlaAlaGl	F;391-	450/Doma
ογ	964 TACTCGCTCGATTATTCATCTCGGGAACCGAGTCAGGAGCTGCTAGTTCA 1014	Alignment Scor Pred. No.:	ent Scor
Dp	160 ValLysLysAlaLeuLysGlnPheGlnAlaGluGlyAspLysAsnAsn 175	Score: Percent	t Simila
δλ	1015 GCCTTTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGATTCTAAT 1068	Best Local	ocal Sin
qq	176GludenProGlnGluProAsnGlnSerThrGlnAspSerSer 189		
ζō	1069 AACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGCATTAGAAGCAAAGAAAACC 1128	7-60-SN	-423-575-
q 0	Glu	ò	457
ζ	1129 CATCTCTTGGATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGTT 1188	QQ	24
Db	210 LysLeuLeuSerMetLeuAspGluValAspArgArgTyrLysGlnTyrTyrGlnGlnMet 229	8	505
ζ	1189 CATACGGTTATATCAGGGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACC 1245	ΩÞ	44
QQ	230 GlnIleValValSerSerPheAspValIleAlaGlyTyrGlyAlaAlaAlaLysProTyrThr 249	λ	550
<i>λ</i> ο	1246 CGGTTTGCCCTCCAAACCGTTTCCTTTATACAAGAACCTGAGAGAGA	qq	64
qa	250 AlaLeuAlaLeuGlnThrIleSerArgHisPheArgSerLeuArgAspAlaIleSerGly 269	ò	610
λŏ	1306 AAGATAATCTCTATGGGATC-TGTATTGGAGAGAGGCAAAGACAAGAC	qq	75
Db	270 GlnileLeuValLeuArgLysCysLeuGlyGluGlnGlnAspGlySerAspGlyLysArg 289	λŏ	670
ò	1353TCAAGAAACCTCTATGTTCCACCAGGATTGCCTTCTTCAGGAGGATGA 1400	qq	91
Db	290 ValGlylleIleSerArgLeuLysTyrVal-AspGlnHisLeuArgGlnGlnArgGl 308	δ	730
<i>λ</i> ο	1401 ACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGT 1460	qq	106
qq	308 yPheMetGlnProGlnAlaTrpArgProGlnArgProGlnVieuProGluAsnSerValLeull 328	à	775
` &	1461 TCTACGGAATTGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAACA 1520	QC	126
QQ	328 eLeuArgAlaTrpLeuPheGluHisPheLeuHisProTyrProLysAspSerAspLysIl 348	ò	811

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-742, 1995
BELL1 gene encodes a homeodomain protein involved in pattern formation in the number: A57632, MUID:96097117, PMID:8521490
A57632
eliminary; not compared with conceptual translation
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                                                                         1626
CACTATGATGATTCCTCAAACAACATGTGGGGTTTTGAAGCAAATAGTGAGTTTCAGGCA 669
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|LeuSerSerAsnProThrSerIleSerLeuGlnSerPheGluLeuArgProGlnGln 145
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                                                                                           GITGAGITCAIGGCICCTCCTCCTCCTCCTCCACTTCATCCTTTGGAICAITTAAGA 609
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rabidopsis thaliana (mouse-ear cress)
eb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
A57632
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4 IleArgMetThrSerClySer------AspHisHisHis
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1-610 <REI>
rences: GB:U39944; NID:g1122532; PIDN:AAB05099.1; PID:g1122533
                                                                                                                                                ----ATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACCA 1674
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DNA binding; homeobox; nucleus; transcription regulation
main: homeobox homology <HOX>
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                                                                         GCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAA-
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GlnGlnGlnGlyTyrSerGlyAsnLysSerThrGlnHisGlnAsnLeuGlnHisThrGln 165
                                                                                                                                                                         LeuSerGluPheCysSerLeuGlyValLysGluSerAspGluGluValMetMetLys
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T02415
probable homeodomain transcription factor [imported] - Arabidopsis thaliana
                            AGATTAGCCTCAGAGCAAGCTTCTTGCAGCAAAGACATTTCTAATAACGTTGTTACT
                                                         MetMetMetMetMetAsnSerHisHisGlnAsnAsnAsnAsnAsnHisGlnHis
                                                                                     CAAGGITTCTCTCTCAACTTATATTTGGC---TCAAAATACCTTCACTCTGTTCAAGAAATA
                                                                                                                                                                                                     ---CGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTT---ACTTCACGTTTTGAGAAT
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340 GlnAlaThrSerGlnAlaLeuGlyGluArgGluGluAspAsnArgAlaValSerIleAla
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|Glu-ThrArgSerGluGlnMetGluIleThr---AsnProMetMetIleAspThrLysPr
                                                                                                                                                                                                                                                               ATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTATATCAGCGTTCCATGCTGCAACCGAGTTA---GATCCACAGTTACACACCCGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .399 AAACGAAAGAACCATCAGATT------TGGAGACCTCAACGAGGTTTGCCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 TrpPheileAsnAlaArgValArgLeuTrpLysProMetileGluGluMetTyrCysGlu
                                                                                                                                             CTATCTCATTTCGCCGCATACTCGCTCGATTATTCATCT--
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N/Alternate names: probable BEL1-like homeotic protein C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Feb-2001 C;Accession: T02415, F84628 F;Accession: T02415, F84628 F;Accession: T02415, F84628 F;Accession: T0241, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Ssubmitted to the EMBL Data Library, May 1998 A;Pescription: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence. A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 A;Accession: T02415 
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139 AsnArgAspMetIleGlyThrValHisValGluGlyGlyLysGlyLeuSerLeuSerLeu :158
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A;Introns: 319/3; 450/2; 470/3
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Best Local Similarity:
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753 AAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTTTCTGATGAATGCTCGGAGATAAG 812	RESULT 11 D84679 probable homeodomain C:Species: Arabidobsi
GASH 240 TCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAGCAAAGACATTTC 872	C;Species: Arabidopsi C;Date: 02-Feb-2001 # C;Accession: D84679
240	M.; Koo, H.; Moffat,
TAATAACGTIGTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTC 932	Nature 402, 751-768, 197 A; Title: Sequence and as A; Reference number: A84
TGTTCAAGAAATACTATCTCATTTCGCCGCATACTCGCTCG	A,Accession: D840/9 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-584 <sto></sto>
	A;Cross-references: GB:
 	A;Gene: At2g2/990 A;Map position: 2
TGATGGTGATTCTAATAACTCGGAGGGGGGTTTCGGATCTAC 1094	Alignment Scores: Pred. No.: Score:
ATTTCAAAGGAGCATTAGAAGCAAAGGAAACCCATCTTTGGATCTTCTCAAATGGT 1154	rercent similarity: Best Local Similarity Query Match: DB:
GGATGATGATAGTCATTGCGTAGATGAGATTCATACGGTTATATCAGCGTTCCATGC 1214	US-09-423-575-1 (1-1886
::: 320 lAspArgArgTyrAsnHisTyrCysGluGlnMetGlnMetValValAsnSerPheAspGl 340	Qy 250 AATCTTCCC
	70
nValMetGlyTyrGlyAlaAlaValProTyrThrThrLeuAlaGlnLysAlaMetSerAr 360 cmmmmchacaaccmcacacacacacacacacaacaacamaarc	Oy 310 AACAACAAC
ArgSerCysGluLeuLe	319
	102
	364
AAAGACAAGAAAAACTCTATGTTCCACCAGCATTGCTTCT 1388	Db 122 AsnGinite
	142
:::: tGluGlnGluAlaTrpArgProGlnArgGlyLeuProGluAr 434	Qy 481 AATTCTATG
AICTGITICGGITCTACGGAATIGGAIGTICCAAAACTICCTICACCCTTACCCGAAAGA 1508	162
gšervalasnīleLeuargalaTrpLeupheGluHisPheLeuasnProTyrProSeras 454	Qy 541 AACCGCAAT
TICGGAGAAACAICTICTAGCTAIACGAAGTGGCTIGACAAGAAGTCAGGTAICAAACTG 1568	182
palaaspiysHisLeuLeualaargGlnThrGlyLeuSerArgasnGlnValSerAsnTr 474	109
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ACCCAACGGACCAACTCTTCGAATGCCGAAAATCTGTTATGATGAGCCAAGCAAT 1/15	מלחבלחזשב 270 ממ

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Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.S.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                        analysis of chromosome 2 of the plant Arabidopsis thaliana.
4420; MUID:20083487; PMID:10617197
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:AE002093; NID:94510417; PIDN:AAD21503.1; GSPDB:GN00139
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ranscription factor [imported] - Arabidopsis thaliana thaliana (mouse-ear cress) equence_revision 02-Feb-2001 #text_change 02-Feb-2001
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rValAlaHisAsnAlaSerAsn-----TrpAsnHis-------
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δ	CGCATACTCGCT	C;Geneti A;Map po
οp	267 ArgPheLeuGluProAlaGlnLysMetLeuGluGluPheCyslleSerTyr 283	A, Intror A, Note:
ò	GAACCGAGTCAGGAGCTGCTAGTTCAGCC	Alignmer
qq		Pred. No Score:
δλ	1039 ATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGGGGGTTTCGGATCTACATTT 1098	Percent Best Loc
qq	294 ThrSerMetGluAspAspAspAspAspAspAspAspLeuSerGlyPheSerSerSerSerSer 313	Query Ma DB:
٥y	-α-	US-09-42
ΩP	314 GluProLeuGluProLysAsnArgLeuLysLysAlaLysLeuLeuPheLeuGln 331	<i>X</i> 0
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Dp	332 GluGluValCysLysTrpTyrLysLeuTyrAsnHisGlnLeuGlnThrValMetSerSer 351	λŏ
δ'n	ATCCACAGTTA CACACCCGGTTTGCCCTCC	qq
QC	352 PheAsnThrValAlaGlyLeuAsnThrAlaThrProTyrIleSerLeuAlaLeuLysArg 371	λδ
δ'n	1264 GTTTCCTTCTTATACAAGAACCTGAGAGAGAGAATCTGCAAGAAGATAATCTCTATGGGA 1323	qa
qq	372 ThrSerArgSerPheLysAlaLeuArgThrAlalleAlaGluHisValLysGlnIleSer 391	ò
δy	AAGACT	qa
Db	 392 SerHisSerSerAsnG1yAsnAsnAsnAsnArgPheGlnLysArgGlnArgSer 409	ò
δλ	1384 CTTCTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGA 1434	qo
Db	410 LeulleGlyAsnAsnValGlyPheGluSerGlnGlnHislleTrpArgProGlnArg 429	ð
δ	1435 GGTTTGCCTGAGAAATCTGTTTTCGGTTTTTTTTTTGGATGTTCCAAAACTTCCTTC	ОЪ
DÞ	430 GlyLeuProGluArgAlaValAlaValLeuArgAlaTrpLeuPheAspHisPheLeuHis 449	λō
ò	1495 CCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGT 1554	qa
Db	450 ProTyrProThrAspSerAspLysGlnMetLeuAlaThrGlnThrGlyLeuSerArgAsn 469	λō
ζŏ	1555 CAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAG 1614	qq
qq	470 GinValSerAsnTrpPhelleAsnAlaArgValArgLeuTrpLysProMetValGluGlu 489	ò
λõ	1615 ATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCC 1665	ପ୍ପ
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δλ	1666 AAC 1668	qq
- QQ	510 Ser 510	ò
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probable	probable homeodomain protein - Arabidonais thaliana	ě

ssion: T48224 n, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew ted to the Protein Sequence Database, March 2000 rence number: Z24488 ssion: T48224 1000 GGAGCIGCTAGTICAGCCTTTACTICACGTTTTGAGAATATAACTGAGTTTCTTGATGGT 1059 .060 GATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGGAGTTAGAAGCA 1119 765 598 GATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGTTTTTGAAGCAAATAGT 657 GAGITICAGGCAȚȚITCAGGȚGTAGITGGȚ------CCAAGTGAACCAATGAIG 705 861 888 143 AlaGlyGluAlaAsnAlaAlaAlaValThrIleAlaSerArgSerSerGlyProLeuGly 162 942 103 SerSerGlyAspValLeuValPheLysProGluProLeuSerLeuSerLeuSerSerHis 122 142 163 ProPheThrdlyTyzAlaSerIleLeuLysGlySerArgPheLeuLysProAlaGlnMet 182 ||| | 51 AspPheLeuAlaAlaGlyGlyPheHisSerAsnAsnAsnAsnAsnAsnHisIleSerAsnPro 70 ------GlyLys 229 90 31 HisProProProProSerSerGlyGlyGlyGlyGlyGlyValPheProLeuAlaAspSer ----CAAGGTITCTCTCAACTIAIAITIGGCTCAAAAIACCTTCACTCTGTTCAAGAA TCTACATTCGGTGAAGAAGATTTCCCGTTTCTAATTTCGAATAAAAGAACAATGAGCTT 766 TCATTGAGTCTTGCATCAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCAGCT 862 AAAGACATTICTAATAACGTIGITACT-----943 ATACTATCTCATTTCGCCGCATACTCGCTCGAT---TATTCATCTCGAGGAACCGAGTCA 826 ACAAGATTAGCCTCAGAG------CAAGCTTCTTGCAGCAGC 532 GITCAAGATAACCGCAATGTTGAGTTCATGGCTCCT----us: preliminary
cule type: DNA
cule type: DNA
cule type: DNA
cule type: DNA
cule 1-575 - ENDE.ALI62508
cimental source: cultivar Columbia; BAC clone T7H20 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: ---CCTCCTCATCCTCCT-------23-575-1 (1-1886) x T48224 (1-575) 223 GlyGlyGlyAspAsn-----4.95e-22 380.00 40.72% 26.58% 11.57% position: 5 ons: 240/3; 374/2; 394/3 : T7H20.80 t Similarity: ocal Similarity: Match: Scores: 568

8 8 8

probable homeodomain protein - Arabidopsis thaliana N;Alternate names: protein T7H20.80 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

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Oy 1120 AAGAAACCCATCTCTGGATCTTCTTCAAATGGTGGATGATATAGTCATTGCGTA 1179		304 GlnGlnGlnCysGlyHisProMetAsnSerGl 1321GGATCTGTATTGGAGAGGGAAAGAAAACAACAA 324 GlyGlySerAspSerSerArgGlyLeuCysSerAl 1378 ÇAȚTGCCTTCTTCAGCAGCTGAAAGGAAAAACAA		Qy 1498 TACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGGGCTTGACAAGAAGTCG 1557	Db 395 VallserAshTiPPHeileAshAlargValargValarpLysProMetValdludluile 414 Qy 1618 TATGCGGAAATGAACAAGGAGGAGCTCAATAACAGTCACAATCAACCAAC		RESOLT 13 H96784 hypothetical protein FIB16.4 [imported] - Arabidopsis thaliana hypothetical protein FIB16.4 [imported] - Arabidopsis thaliana (S.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C.Accession: H96784 Fireologis, A., Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.	urs: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, M.; Rooney, T.; Rowdey, D.; Saxano, H. M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, i.st., Schwarce, and analysis of chromosome 1 of the plant Arabidopsis. secon: H96784 s: preliminary us: preliminary us: preliminary uses: l-292 < STO> uses: DAA uses: L-292 < STO> uses: GB:AE005173; NID:g10120438; PIDN:AAG13063.1; GSPDB:GN00141	C;Genetics: A;Gene: F1B16.4 A;Map position: 1

Ongs to the nscription. Db 296 ed.hHisteumetHisProTyrProThrdluAspdluLysArgGlnIleAlaAladinTh 316 Qy 1539 TGGCTTGACAAGAGTCAGCTATCAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAA 1598 L	Oy 1653 TCACATTCAACCCAACGGACCAACTCTTCGAATGCCAAAATCTGTT 1698 Db 356 nHisArgProThrGlnArgPheTrpProAsnSerIle 368 RESULT 15 \$42543 Nyochhetical protein - soybean	C;Species: Glycine max (soybean) C;Dacabal 1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999 C;Dacabal 1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999 C;Accession: 842543 R;Ma, H.; McMullen, M.D.; Finer, J.J. Plant Mol. Blol. 24, 465-473, 1994 A;Title: Identification of a homeobox-containing gene with enhanced expression during A;Reference number: 842543; MUID:94169300; PMID:7907232 A;Accession: 842543; MUID:94169300; PMID:7907232	A.Molecule from MAA A.Residues: 1-379 «MAH» A.Residues: 1-379 «MAH» A.Cross-references: EMBL:L13663; NID:g310568; PIDN:AAA20882.1; PID:g485406 C.Superfamily: unassigned homeobox proteins; homeobox homology C.Keywords: DNA binding; homeobox; nucleus; transcription regulation F;284-343/Domain: homeobox homology «HOX»	Alignment Scores: 5.42e-06 Length: 379 Score: 177.00 Matches: 92 Percent Similarity: 35.31\$ Conservative: 69 Best Local Similarity: 20.18\$ Mismatches: 141 Query Match: 5.39\$ Indels: 154 DB: 20 US-09-423-575-1 (1-1886) x S42543 (1-379)	Qy 298 AACCCAATGGACAACAACAACAACAACAACACACTTTTAGTTCTCTGGATAATGTCATGACT 357 ::: ::::: :::		2, 4 4, 7 4, 6 5, 3, 8	Db 86 AspAsnAsnThrGlyLeuGlyTyrTyrPheMetGluSer 100 Qy 583 CCACTTCATCCTTTGGATCATTTAAGACACTATGATGATCCTCAAACAACAACATGGGGT 642	Qy 643 TTTGAAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGCTCCAAGTGAACCAATG 702
C;Comment: This protein, functions as a nuclear transcription factor that belongs and interacts with PBX proteins and plays a tissue-specific regulation of transcr A;Gene: pknox2 A;Gene: pknox2 A;Map position: chromsome 11q24 Alignment Scores: Pred. No.: 186.50 Matches: Percent Similarity: 44.08 Matches: Percent Similarity: 42.58 Mismarches: Rismarches: h: 5.68\$ Indels: 75 2 Gaps: 14 575-1 (1-1886) x JC7766 (1-460) 811 AGTCTTTGCAGCTACAAGATTAGCCTCAGAGCAAGACATT 61	** SerLysalacinalavalHisileSerAlaProSerAlaAlaAlaAlaSerThrProvalPro 45 871 TCTAATAACGTTGAGGTTTCTCCAACTTATATTTGGCTCAAATACCTTGAC 930 **:	ACCGAGTCAGGAGCTGCTAGCCTTTACTTCACGTTTTGAGAATATAACTGAGTTT	101 ValHisGlnGlnGluGlnGluHisLysProPhePheSerAspAspProGluLeuAspAsn 120 1096 TTTCAAAGGGAAGGAAAAACCCATCTTTGGATCTTTCAAATGGTG 1155 1156 GATGATCGATATAGGAAAGAAAAACCCATCTTTTGGATCTTTTTAAATGGTG 1155 1156 GATGATCGATATAGTCATTGCGTAGATTCATACGGTTATATCAGGTTTC 1209 1156 GATGATCGATATAGTCATTGCGTAGATTCATACGGTTATATCAGGTTTC 1209 1150 ASHGIULeuCysLysAspPheCysAshArgTyrIleThrCysPheLysThr 156	1210CATGCTGC-AACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCT 1256	1257	AlaMetThrThrValAsnSerGlnValValSerGlyGlyAlaLeuTyrGlnProValThrTGAAGAAACCTGTATGTTCCACGAGCATTGCCTTCTTCAGCAGCTGAAACG	237 MetValThrSerGlnGlyGlnValValThrGlnAlalleProGlnGlyAla-IleGlnIl 256 1404 AAAGAACCATCAGATTTG 1421 :::	1422 GAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTGGATGTT 1478 ::: :: ::: ::: ::: ::: 276 rLysAsnLysArgGlyValLeuProLysHisAlaThrAsnIleMetArgSerTrpLeuPh 296	

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145	822	164	873	դ. Հ	933	6	208	1053	227	1113	237	1173	242	1227	253	12	262	1344	276	1404	283	1464	298	1524	318	1584	338		
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Search completed: September 2, 2004, 12:13:05 Job time : 61 secs

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OM nucleic - protein search, using frame_plus_n2p model

September 2, 2004, 09:48:42; Search time 22 Seconds (without alignments) 8927.665 Million cell updates/sec BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext Title: Perfect score: Scoring table: Sequence: Run on:

283362

141681 segs, 52070155 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P48731 arabidopsis	070477 mus musculu	P55347 homo sapien	Q60954 mus musculu	_	P97367 mus musculu	000470 homo sapien	P97368 mus musculu	P79937 xenopus lae	096kn3 homo sapien		P46608 glycine max	022299 Iycopersico	P48000 arabidopsis	Q43484 hordeum vul	Ognoc8 homo sapien	-	
SUMMARIES		ID	ATH1 ARATH	PNX1_MOUSE	PNX1 HUMAN	MEI1 MOUSE	MEI2 HUMAN	MEI2 MOUSE	MEI1 HUMAN	MEI3 MOUSE	MEI1 XENLA	PNX2 HUMAN	MEI3 HUMAN	HMB1 SOYBN	HKL6 LYCES	HKL3 ARATH	KNX3 HORVU	SIX2 HUMAN	HKL1 MALDO	HKN1_MAIZE
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		Score	2484	208	202	196.5	196.5	196.5	195.5	194	189.5	186.5	182	177	175.5	175.5	169.5	169	167	166.5
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MGD; MGI:1201409; Pknox1.
MGD; MGI:1201409; Pknox1.
MGD; GO:000567; C:transcription factor complex; IDA.
GO: GO:00051705; F:protein binding; IPI.
GO; GO:0003705; F:protein binding; IPI.
GO; GO:0006357; P:regulation of transcription from Pol II pro.
InterPro; IPR001256; Homeobox.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein PKNOXI (PBX/knotted homeobox 1)
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Pfam; PF00046; homeobox; 1.
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95 PheValArgLysGlnGluLysAspGlyLysProPhePheCysGluAspProGluThrAsp 114
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210 ValfyrGlnProValThrValValThrProGlnGlyGlnValValThrGlnAlaLeuSer 229
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|IeGlnSerAlaileThrGly------ThrLeuSerProGlnGlyIleVal
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SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMBOBOX 1; FALSE_NEG.
PROSITE; PS50071; HOMBOBOX 2; 1.
HOMBOBOX; DNA-binding; Nuclear protein.
DNA BIND 258 320 HOMBOBOX (TALE-TYPE).
SEQÜENCE 435 AA; 47395 MW; 354369A1795A1E84 CRC64;
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Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Bark H.-S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,
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Thours sequence of human chromosome 21.";
Mature 405:311-319(2000).
--- SINGLARITY: Belongs to the Talls/MEIS homeobox family.
                               AACTICCTICACCCITACCCGAAGAITCGGAGAAACAICTICTAGCTATACGAAGTGGC 1542
                                                                                                                                                                                                                           320 MetLeuAspSerSerCysSerGluThrProLysThrLysLysLysProAlaGlnAsnArg 339
                                                                              340 ProvalGlnArgPheTrpProAspSerLeuAlaSerGlyValAlaGlnAlaThrProSer 359
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P55347; 000528;
P1-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein PKNOX1 (PBX/Knotted homeobox 1) (Homeobox protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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360 GluLeuAlaMetSerGlu 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1033 GAGAATATAACT----GAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 ---AlaGluGlyValSerProProProValGluSerGlnThrProMetAspValAspLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1147 CAAATGGTGGAT-------GATCGATATAGTCGTA-----
                                                                                                                                                                                                                                                                                                                                                                                    .
ta
                                                                                                                                                                                                                                                                                                                                                              MIM; 602100; -.
GO; GO:0003704; F:specific RNA polymerase II transcription :
GO; GO:0003700; F:transcription factor activity; TAS.
IIILEFPC; IPROUSONS: DAMPODOX.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> E (IN REF. 2).
-> A (IN REF. 1).
-> A (IN REF. 2).
BOF582F0A3E1CAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 GTTACTCAAGGTTTCTCTCTCAACTTATATTTGGCTCAAA---
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Matches:
Conservative:
Mismatches:
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PROSITE; PS00027; HOMEOBOX 1; FALSE_NBG.
PROSITE; PS50071; HOMEOBOX 21; FALSE_NBG.
PMA-binding; Nuclear protein; Homeobox.
DNA_BIND 258 320 HOMEOBOX (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-423-575-1 (1-1886) x PNX1_HUMAN (1-435)
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202.00
41.03%
23.10%
6.15%
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429
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Best Local Similarity:
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346
429
435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 CATCCTCCTCCACTT----CATCCTTTGGATCATTTAAGACACTATGATGATTCCTCA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SER/THR-RICH.

SER/GUL-RICH (ACIDIC).

POLY-ASP
HOMEOBOX (TALE-TYPE).

HOMEOBOX (TALE-TYPE).

BASSMOKUMANDREGGMHYM -> LQSWPGEYVARGGPMGVSM
GQPSYTOAQMPPHPAQLRHGPPMHYYLPGHPHPPAYMHGG
OPHPGMPMSASSPSYLNTGDPTMSAQVMDIHAQ (in
  IsoId=C60954-2; Sequence=VSP_002240;
-!-TISSUE SPECIFICITY: Expressed at high levels in the lung with lower lower bedeected in the heart and brain.
-!- DEVELOPMENTAL STACE: Expressed at high levels in all stages of embryonic development analyzed (7 days to 17 days).
-!- INDUCTION: Expression is coactivated by retroviral integration in EXH-2 murine myeloid leukemiae as a site of viral integration in 15% of the tunors arising in EXH-2 mice that develop myeloid leukemia as a result of the expression of an ecotropic murine leukemia as a -!- SIMILARITY: Belongs to the TALE/METS homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisGlyProProLeuHisSerHisGlnTyrProHisThrAlaHisThrAsnAlaMetAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ProSerMet --- GlySerSerValAsnAspAlaLeuLysArgAspLysAspAlaIle---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005667; C:transcription factor complex; IDA.
GO; GO:0003667; E:transcription factor complex; IDA.
GO; GO:0003515; F:DNA binding; IDA.
GO; GO:0003515; F:RNA polymerase II transcription factor acti.
GO; GO:0008357; P:regulation of transcription from Pol InterPro; IPR001356; Homeobox; I.
Probom; PD00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; FALSE NEG.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Nuclear protein; Homeobox; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 002240.
E0C32B5CE25E1E2C CRC64;
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Matches:
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EMBL; U33630; AAA85509.1; --
HSSP; P40424; 1B72.
TRANSFAC; T03389; --
TRANSFAC; T03389; --
MGD; MGI: 104717; Meis1.
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196.50
37.40%
24.68%
5.98%
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VARSPLIC
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                                                                                                                                                             ---TICTIAȚACAAGAACCTG------AGAGAGAGAGAATCTGCAAGATA 1311
                                                                                                                                                                                                                                                  -----GACAGACTCAAGAA 1359
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318 GlnProMetLeuAspSerSerCysSerGluThrProLysThrLysLysLysThrAlaGln 337
                         TTACACACCGGTTTGCCCTCCAAACCGTTTCC---
                                                                                                                                                                                         GlyThrValTyrGlnProValThrValValThrProGlnGlyGlnValValThrGlnThr
                                                                                                                                                                                                                                                                     1180 GATGAGATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAG---
                                                                                                       |||::: ||||||:::
188 IleValValProAlaSerAlaLeuGlnGlnGlyAsnValAlaMetAlaThrValAlaGly
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|LeuSerIleLeuHisGln------AspAspGlySerSerLysAsn-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   338 AsnArgProValGlnArgPheTrpProAspSerIleAlaSerGlyValAlaGlnProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell. Biol. 15:5434-5443 (1995).
-!- FUNCTION: May function as a cofactor for HOXA7 and HOXA9 in the induction of myeloid leukemias.
-!- SUBCELLUJAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEII MOUSE STANDARD; PRT; 390 AA.
Q60954; Q60955;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meis! (Myeloid ecotropic viral integration site-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — SEQUENCE FROM N.A. (ISOFORMS MEISIA AND MEISIB). MEDLINE=96009570; PubMed=7565694; Moskow J.J., Bullrich F., Huebner K., Daar I.O., Buchberg A.M.; Meisi, a PEXI-related homeobox gene involved in myeloid leukemia EXH-2 mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEISI.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                           1312 ATCTCTATGGGATCTGTATTGGAGAGAGGCAAA----
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IsoId=Q60954-1; Sequence=Displayed;
Name=MeislB;
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                                                                                                                                                                                                                                                                                                                      171 HisArgTyrlleSerCysLeuLysGlyLysMetProlleAspLeuVallleAspAspArg 190
                                                                                                                                                                                                                                                                                                                                                                             840
                                                                                                 111 ValĊysserSerGluserPheAsnGluAspIleAlaValPheAlaLysGlnIleArgAla 130
                                                                                                                                                                ||||::: ||||| ||||| GluLeuPheSerSerAsnProGluLeuAspAsnLeuWetIleGlnAlaIleGln 150
                                PheGluLysCysGluLeuAlaThrCysThrProArgGluProGlyValAlaGlyGlyAsp 110
                                                                                                                                                                                                               CAACTTATATTTGGCTCAAAATACCTTCACTCTGTTCAAGAAATACTATCTCATTTC--- 957
                                                                                                                                                                                                                                                                                    --GCCGCATACTCGCTCGATTATTCATCTCGAGGAACC 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 ---LysArgHisLys-------LysArgGlyIlePheProLysValAlaThrAsn
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                                                                  ----TGTGCAGCTACAAGATTAGCCTCA
                                                                                                                                           GAGCAAGCTTCTTGCAGCAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTCT
AAAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTT--
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                                                                      GAATGCTCGGAGATAAGTCTT----
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MEI2 HUMAN STANDARD; PRT; 477 AA. O14770; Q96KI4; Q96KI5; Q9NRS1; Q9NRS2; Q9NRS3;

HUMAN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOId=014770-5; Sequence=VSP 002243, VSP 002244; TISSUE SPECIFICITY: Expressed in various tissues. In hematopoietic tissues, the lymphoid organs express high levels of MEIS2. Also expressed in some regions of the brain, such as the putamen. SIMILARITY: Belongs to the TALE/MEIS homeobox family. SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                TISSUE=Erain;
MEDLINE=20347166; PubMed=10764806;
Yang Y., Hwang C.K., D'Souza U.M., Lee S.-H., Junn E., Mouradian M.M.;
"Three-anino acid extension loop homeodomain proteins Meis2 and TGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSP_002245, VSP_002246;
                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS MEIS2A; MEIS2B; MEIS2C; MEIS2D AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE OF 271-477 FROM N.A. (ISOFORM MEIS2B).
MEDLINE-98051942; PubMed-9383298;
Smith J.E. Jr., Afonja O., Yee H.T., Inghirami G., Takeshita "Chromosomal mapping to 15q14 and expression analysis of the MEIS2 homeobox gene.";
Mamm. Genome 8:951-952(1997).
                                                                                                                                                        Craniata; Vertebrata; Butele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=014770-2; Sequence=VSP_002245; VSP_002246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
        15-WAR-2004 (Rel. 40, Last sequence update)
Homeobox protein Meis2 (Meis1-related protein 1).
MEIS2 OR MRG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=014770-4; Sequence=VSP_002242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=014770-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                            differentially regulate transcription.";
J. Biol. Chem. 275:20734-20741(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                              Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates;
                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Meis2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Meis2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Meis2A;
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                                                                                                                                          Homo sapiens
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Db 78 AspalaileTyrGlyHisProLeuPheProLeu 88 Qy 736 CTAATTTCGAATAAAGAAACAATGAGCTTTCATTGAGT774 Db 89 LeuAlaLeuValPheGluLysCysGluLeuAlaThrCysThrProArgGluProGlyVal 108	Oy 775 CTTGCATCAGATGTTTCTGATGAATGCTGGAGATAAGTCTTTGTGCAGCTACA 82	Qy 829 AGATTAGCCTCAGAGCTTCTTGCAGCAAGCAAAGACTTTCTAATAACGTTGTTACT 88	Qy 889 CAAGGITICTCTCAACTTAATTITGGCTCAAAATACCTTCACTGTTCAAGAAATACTA 94	OY 949 TCTCATTTCGCCGCATACTCGCTC972 ::: ::: Db 169 AspasnPheCy8HisArgTyxIleSerCysLeuLysGlyLysMetProlleAspLeuVal 188	Qy 973GATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTT 102		Qy 1081 GGTTTCGGATCTACATTTCAAAGGAGAGCATTAGAAGAAAACCCATCTTGGAT 114	Qy	Qy 1201 TCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAA 1260 ::::: Db 260 AlaSerProGlyThrGlyAspAspAspAspAspProAsp	1261 ACCGTTTCCTTCTTATACAAGAACCTGAGAGAGAGAATCTGCAAGAAGATAATCTCTATG	OY 1321 GGATCTGTATTGGAGAGGCAAAGACTCAAGAAACCTCTATGTTCCACCAGGT 1380 Db 272	QY 1441CCTGAGAAATCTGTTTCGGTTCTAGGAAATTGGATGTTCCAAAACTTCCTTC	Oy 1558 GTATCAAACTGGTTTATAAATGCGCGGGTTAGGAAGCCGATGATAGAAGG 1614
11 to license@isb-sib.ch). AAF81639.1; AAF81640.1; AAF81641.1;	AAH50431.; AAB70270.1;		уmerase	Filtranscription co-repressor activity; TAS. 1956; Homeobox. oneobox; 1.	E_NEG.	HOWENDOX; MAY DIMINING NUCLEAR PROCEDUR; ALCETNATIVE SPLICING. DOMAIN 246 273 ASP/GLU-RICH (ACIDIC). DOMAIN 266 273 POLY-ASP. FOLY ASP (AND STATE NICH).	DOA (IALE-TIFE). Ing (in isoform Meis2B D). ENSP 002242.	hr -> v (in 180form m /FTId=vSp 002243. Missing (In isoform Me /FTId=vSp 002244.			: 1.18e-07 Length: 477 196.50 Matches: 90 ty: 33.89\$ Conservative: 52 arity: 21.48\$ Mismatches: 152 1 Indels: 125 (1-1886) x MEIZ_HUMAN (1-477)	GCTTTGATATTTTCAATTCTATGCTGACTAACAAATACTTATCATCTTCTCCA	ATGETOLIE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retinoic
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS MEIS2A; MEIS2B; MEIS2C AND MEIS2D).
MEDLINE=97477074; PubMed=9337137;
Oulad-Abdelghani M., Chazaud C., Bouillet P., Sapin V., Chambon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P97367-2; Sequence=VSP_002248, VSP_002249;
Name=Meis2B; Synonyms=Mrg1A;
IsoId=P97367-3; Sequence=VSP_002247, VSP_002248, VSP_002249;
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                      STRAIN=Swiss Webster;
MEDLINE=91108670; PubMed=8950991;
Nakamura T., Jenkins N.A., Copeland N.G.;
"Identification of a new family of Pbx-related homeobox genes.";
                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A. (ISOFORMS MEIS2B/MRGIA AND MEIS2D/MRGib).
MEDLINE=97202105; PubMed=9049622;
Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
"Identification of a conserved family of Meisl-related homeobox
                                                                                                                                                                                                                                                                                                                                 "Meis2, a novel mouse Pbx-related homeobox gene induced by retiracid during differentiation of P19 embryonal carcinoma cells.";
Dev. Dyn. 210:173-183(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bvent=Alternative splicing, Named isoforms=4;
Comment=Additional isoforms seem to exist;
 15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meis2 (Meis1-related protein 1).
MEIS2 OR MRG1 OR STRA10.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 7:142-156(1997).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM MEISZA)
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EMBL; AJ000505; CAA04139.1; --
EMBL; AJ000506; CAA04440.1; --
EMBL; AJ000507; CAA04141.1; --
EMBL; U68383; AAB19193.1; --
EMBL; U68384; AAB19194.1; --
HSSP; P40424; 1B72.
TRANSFAC; T03405; --
TRANSFAC; T03407; --
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EMBL; AJ000504; CAA04138.1; -
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| SInValArgAlaGluLysProLeuPheSerSerAsnProGluLeuAspAsnLeuMetlle 148
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                                                                                                                                                                                                                                                                                                                                   /FTIGEVSP_002247.
LOSMPGDYSQGDPMGMG -> PMSGMGNNMGMDGQWHYM
(in isoform Meis2A and isoform Meis2B).
/FTIGEVSP_002248.
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                                                                                                                                                                                                                                                                              HOMEOBOX (TALE-TYPE).
Missing (in isoform Meis2B and isoform
                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_002248.
Missing (in isoform Meis2A and isoform
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SER/THR-RICH.
ASP/GLU-RICH (ACIDIC).
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-> A (IN REF. 1).
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Matches:
Conservative:
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                                MGD; MGI:108564; Mrgl.
GO; GO:0003677; F:DNA binding; IDA.
GO; GO:0001654; P:eye morphogenesis; IGI.
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                                                                                  InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX; 1.
PROSITE; PS00027; HOMEOBOX 2; 1.
DNA-binding; Nuclear protein; Homeobox 1.
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33.89%
21.48%
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T03408; -. T03409; -.
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316
477 AA;
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Best Local Similarity:
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256
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346
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RX MEDLINE=22388257; PubMed=12477932;

Rt Atasner R.D., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,

RA Altasner R.D., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,

RA Altasner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Rad Acchence L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Soares M.B., Mullahy S.J.,

RA Brak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hilalon D.K., Muzhy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation Sci. U.S.A. 99:1689-16903 (2002).

--- TISSUE SPECIFULIAR LOCATION: Nuclear (Probable).

--- TISSUE SPECIFULIAR LOCATION: Nuclear (Probable).

--- TISSUE SPECIFULIAR LOCATION: Nuclear (Probable).

--- TISSUE SPECIFULIY: Expressed at low level in normal immunohapatopoietic tissues, including the fetal liver. Expressed to my subset of myeloid Leukemia cell lines, with the highest excression seen in those with a megakaryocytic-erythroid phenotype.

--- SIMILARITY: Selongs to the TALE/MEIS homeobox family.

--- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; I.O.DNA-binding; Muclear protein; Homeobox; DOMALN 194 240 SER/THR-RICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-423-575-1 (1-1886) x MEI1_HUMAN (1-390)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U85707; AAC51642.1; -. EMBL; BC043503; AAH43503.1; HSSP, P40424; 1B72. TRANSFAC; T03419; -. Genew; HGNC:7000; MEIS1.
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195.50
37.40%
24.68%
5.95%
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334
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262
272
390 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAA 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 ACCGTTTCCTTCTTATACAAGAACCTGAGAGAAGAATCTGCAAGAAGATAATCTCTATG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCCGAAAGATTCGGAGAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAG 1557
                                                                                                                                                                                                                                                                                                                                                                                                    244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 PheProLysValAlaThrAsnIleMetArgAlaTrpLeuPheGlnHisLeuThrHisPro 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||| ::: :::|||
TyrProSerGluGluGlnLysLysGlnLeuAlaGlnAspThrGlyLeuThrIleLeuGln 322
     GlnAlaileGlnValLeuArgPheHisLeuLeuGluLeuGluLysValHisGluLeuCys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATCAAACTGGTTTATAAATGCGGGGTTAGGCTATGGAAGCCGATGATAGAAGAG 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTT
                                                                                                                                                                                            189 IleAspGluArgAspGlySerSerLysSerAspHisGluGluLeuSerGlySerSerThr
                                                                                                                                                                                                                                              1021 ACTICACGITITIGAGAATATAACTGAGITICTIGATGGIGATICTAATAACTCGGAGGCG
                                                                                                                                                                                                                                                                               1321 GGATCTGTATTGGAGAGAGAGAAAGACAAGACTCAAGAAACCTCTATGTTCCACCAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97369938; PubMed=9226379;
Smith J.E. Jr., Bollekens J.A., Inghirami G., Takeshita K.;
"Cloning and mapping of the MEIS1 gene, the human homolog of a murine
leukemogenic gene.";
                                                                                                    AspAsnPheCysHisArgTyrIleSerCysLeuLysGlyLysMetProIleAspLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            |||:::
|SerAlaGlyThrProGlyProSerSerGlyGlyHisAlaSerGlnSer-----
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260 AlaSerProGlyThrGlyAspAspAspAspProAsp-------
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15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meisl.
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                                                 949 TCTCATTTCGCCGCATACTCGCTC---
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Genomics 43:99-103(1997)
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TISSUE=Uterus;
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000470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 HisGlyProProLeuHisSerHisGlnTyrProHisThrAlaHisThrAsnAlaMetAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCCTCCTCCACTT-----CATCCTTTGGATCATTTAAGACACTATGATTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628 AACAACATGTGGGGTTTTTGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGT
                                                                                                                                                                                                                                                                                                      Genew, HGNC:7000; MELSI.

MIM; 601739; --
GO:0003702; F:NA polymerase II transcription factor acti.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
ProDom; PD00010; Homeobox; 1.
SMART; SM0389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
Homeobox; Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SER/THR-RICH.
ASP/GLU-RICH (ACIDIC).
POLY-ASP.
HOWEOBOX (TALE-TYPE).
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97
1144
102
140
140
140
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AspGluLeuArgHisTyrProGly1leThrGluHisThrThrAlaLeuAlaSerPheSer 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AlaAlaProServalProArgAlaProGlyProTyr 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGGTTTTGAAGCAAATAGT
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung.
DEVELOPMENTAL STAGE: Not expressed until 11 days in embryonic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the TALE/NEIS homeobox family. SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER/THR-RICH.
ASP/GLU-RICH (ACIDIC).
HOMEOBOX (TALE-TYPE).
; 2175D0F4341E24B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                            6
                                                                                         15-JUL-1998 (Rel. 36, Created)
10-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meis3 (Meis1-related protein
MEIS3 OR MRG2.
346 ThrProTyrAsnProAspGlyGlnProMetGly 356
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC, T03406; -.
MGD; MG1:108519; Mrg2.
InterPro; IPR001356; Homeobox.
Ffam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SNART; SM00389; HOK; 1.
PROSITE; PS00027; HOMEOBOX 1; FALSE NEG.
                                                                      378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-423-575-1 (1-1886) x MEI3_MOUSE (1-378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homeobox.
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232 S
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HSSP; P40424; 1B72.
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194.00
34.38%
23.15%
5.91%
                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 AA;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
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                                                         588 CCAAGTGAACCAATGATGTCTACATTCGGTGAAGAAGATTTTCCCGTTTCTAATTTCGAAT 747
                                                                                                                              748 AAAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTT-------TCTGAT 795
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     -----TyrclyHisProLeuPheProLeuLeuAlaLeuIle
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IDS 111	P7937; P7938; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence v 10-OCT-2003 (Rel. 42, Last annotation Homeobox protein Maisl (KNeisl). Xenopus laevis (African clawed frog). Eukaryote, Metazoa; Chordata; Cranial Amphibia; Batrachia; Anura; Mesobatra Xenopodinae; Xenopus. [1]	RP SEQUENCE FROM N.A. (ISOPORMS MEIS1-1 AND MEIS1-2). RA MEDLINE=97202105; Pubmed=9049632; RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T., RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.; RT "Identification of a conserved family of Meis1-related homeobox RT Genome Res. 7:142-156(1997). CC -!- SUBCELULIAR LOCATION: Nuclear (Probable). CC -!- ALTERNATIVE PRODUCTS. CC ALTERNATIVE PRODUCTS. CC ALTERNATIVE PRODUCTS. CC ALTERNATIVE PRODUCTS. CC ALTERNATIVE PRODUCTS. CO SPORT-Alternative splicing, Named isoforms=2; CC COMMENT-Additional isoforms seem to exist;	This the was a control of the contro	DR EMBL; U68386; AAB19196.1; - DR HSPP; P41778; 1DU6. DR TRANSFAC; T03390; - TRANSFAC; T03391; - DR TRANSFAC; T03391; - DR TRANSFAC; T03391; - DR TRANSFAC; T03391; - DR PRODUM; PF001356; Homeobox; 1. DR PCDCM; P500010; Homeobox; 1. DR PCSTTE; P600027; HOMEOBOX 1; FALSE_NEG. DR PROSITE; P600027; HOMEOBOX 2; 1. DR PROSITE; P600027; HOMEOBOX 2; 1. DR PROSITE; P600027; HOMEOBOX 2; 1. DR PROSITE; P600027; HOMEOBOX 2; 1. DR PROSITE; P600027; HOMEOBOX 3; 1. DR PROSITE; P600027; HOMEOBOX 1; FALSE_NEG. FT DOMAIN 194 269 POLY-ARF. FT DOMAIN 242 269 POLY-ARF. FT HOMEOBOX (TALE-TYPE). FT VARSPLIC 373 390 PAGPORTISASPENTATEDEMMANGG PPOPORTISASPENTATEDEMMANGG PPOPORTISASPENTATEDEMMANGG PPOPORTISASPENTATEDEMMANHAQ (in isoform Meisl-2). FT VARIANT 34 34 K -> Q (IN MEISL-2).
705 70 Thr ProHis Arg ProproGlu Leugland Leugh Leugh Serbap Ser Leulys Arg 58 706 TCTACATTCGGTGAAGAGATTTCCGTTTCTAATTTCGAATAAAGAAC 75 1::	99 G1yG1yAspValCySSerSerAspSerPheAsnG1uAspIleAlaAlaPheAlaLySG1n 118 832 TTAGCCTCAGAGCAACCTTCTTGCAGCAAGAAGACATTCTAATAACGTTGTTACTCAA 891 :::	159 1012 161 161 1072	1 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1330 TTGGGGAAGCAAGACTCAAGAAACCTCTATGTTCCACCACGTTGCCTTCTT 242

1212 TGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAAACCGTTTCCTT 259 TThxGlyAspAspAspAspPro	Db 266	ATCTGTTTCGGTTCTACGGAATTGGATGTTCC :::	Db 302 uGluGinLysLysGlnLeuhlaGlnaspThrGlyLeuThrIleLeuGinValasnashfr 322 Qy 1569 GTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAAT 1628 Db 322 pPhelleAsnAlaArgArgArglleValGlnProMetIleAspGlnSerAsnArgAlaVa 342 Ov 1629 GBACAAAGGGAAGCTCAAATAACAGTTCAACCGAACGGA 1671	1017 GENERAL CARLING CARGO CONTROL CARGO CONTROL CARGO CONTROL CARGO CONTROL CARGO CONTROL CARGO CONTROL CARGO CONTROL CARGO C		UB PKBV2.1. GN PKNOXO PREP2. OS Homo saplens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NN NCBI TaxID=9606;			Blochem, Blophys, Res. Commun, 287:27 -!- SUBCELLULAR LOCATION: Nuclear. -!- SIMILARITY: Belongs to the TALES/M -!- SIMILARITY: Contains 1 homeobox d	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation CC the European Bloinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).
FT VARIANT 91 91 F -> L (IN MEIS1-2). FT VARIANT 178 178 E -> K (IN MEIS1-2). FT VARIANT 273 N -> H (IN MEIS1-2). FT VARIANT 275 275 G -> K (IN MEIS1-2). FT VARIANT 315 315 MISSING (IN MEIS1-2). SQ SEQUENCE 390 AA, 42887 MW, DOD986782F CRC64;	Alignment Scores: 4.02e-07 Length: 390 Pred. No.: 189.50 Matches: 99 Score: 18.50 Matches: 99 Bercent Similarity: 26.09% Conservative: 58 Best Local Similarity: 22.76% Mismatches: 156 Query Match: 1.77% Indels: 153 DB: 15	US-09-423-575-1 (1-1886) x MEIL_XENLA (1-390) Qy 460 ATGGGTGGCTTTGATATTTCAATTCTATGCTGACTAACAAAACTTATCATCTTCTCCA 519 Qy 1400 ATGGGTGGCTTTGATATTTCAATTCTATGCTGACTAACAAAAACTTATCATCTTCTCCA 519	34 LygSerValHisHisheuAsnHisGly 42 580 CCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATCCTCAAACAAC 63	OY 634 ATGTGGGGTTTTGAAGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTTGGTCCAAGT 693 by 694 GAACCAATGATGAGTGAAGAAGATTTCCGGTTTCTAATTTCGAATAAAAGA 753 cy 694 GAACCAATGATGTCTACATTCGGTGAAGAAGATTTCCCGTTTCTAATTTCGAATAAAAGA 753 ch 73 Arganiyasangatgtctaagatgaagaagaagattagaagaagaagaagaagaaga	754 AACAATGAGCTTTCATTGAGTCTTGCATCAGATGTTTCTGATGAATGC	Qy 802 TCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAA 846	133 ProLeuPheSerSerAsnProGluLeuAspAsnLeuMetIleGlnAlaileGlnValLeu 907 ATAITTGGCTCAAAATACCTTCACTCTGTCAAGAAATACTATCTCATTTC 153 ArgPheHisLeuLeuGluLeuGluLysValHisGluLeuCysAspAsnPheCysHisArg	OY 958	OY 1056TGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCA 1100	Qy 1101 AAGGAGACCATTAGAAGGAAAGCCGATCTCTTGGATCTTCTTCAAAT 1151 Db 220 AlaAlaSerIleArgSerGlyGlyThrProGlyProSerSerGlyGlyHisThrSerHis 239 Qy 1152 GGTGGATGATCGATAGTCATTGCGTAGATGAGATTCATACGGGTTATATCAGCGTTCCA 1211

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This SWISS-PROT entry is copyright: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     1462 CTACGGAATTGGATGTTCCAAAACTTCCTTCACCTTACCCGAAAGATTCGGAGAAACAT 1521
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                                     -ACCTCTATGTTCCACCAGCATTGCCTTCTTCAGCAGCTGAAACGA
                                                                                         261 ValAsnLeuAspLeuThrSerLeuLeuAspAsn-------GluAspLysLysSer
                                                                                                                                             AAGAACCATCAGATTTGGAGACCTCAACGAGGT----TTGCCTGAGAAATCTGTTTCGGTT
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SEQUENCE OF 175-382 FROM N.A.
MEDLINE=97202105, Pubmed=9049632;
Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
"Identification of a conserved family of Meisl-related homeobox
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299687; 387PW2;
15-UDI-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HOMEODOX protein Meis3 (Meisl-related protein 2) (Fragment)
MEIS3 OR MRG2.
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Catarrhini; Hominidae; Homo.
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Go, GO:0005634; C:nucleus; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GATGAGATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAG 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValHisGlnGlnGluGlnGluHisLysProPhePheSerAspAspProGluLeuAspAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 AspAsnLeuLeuArgAsnAspLeuGlyGlyProTyrSerProAsnGlnProSerIleAsn 180
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241 GlnGlyGlnValValThrGlnAla1leProGlnGlyAla1leGlnIleGlnAsnThrGln 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 ValAsnSerGlnValValSerGlyGlyAlaLeuTyrGlnProValThrMetValThrSer 240
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG. PROSITE; PS50071; HOMEOBOX_2; 1. HOMEOBOX; DNA-binding; Nuclear protein. DNA_BIND 279 338 HOMEOBOX.
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POLY-PRO.
POLY-GLU.
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EMBL; AJ417081; CAD01142.1; -.
EMBL; AB065001; BAB8365.1; -.
TRANSFAC; T05155; -.
Genew; HGNC.16714; PKNOX2.
InterPro; IPR001356; Homeobox.
ProDom; PR00046; homeobox; 1.
ProDom; PM0001010; Homeobox; 1.
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186.50
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460 AA;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                DOMAIN
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	CC -:- FUNCTION: Possible transcription activator involved in early cembryonic development. Probably binds to the DNA sequence 5'-TGAC-CC 3'- SUBCELLUAR LOCATION: Nuclear (Probable). CC -:- SUBCELLUAR LOCATION: Expressed mainly in embryonic tissues. Weakly detected in stems and hypocotyl. CC -:- DEVELOPMENTAL STAGE: First expressed in the embryo proliferation crage, increases during early somatic embryo development and decreases thereafter. CC decreases thereafter. CC -:- SIMILARITY: Belongs to the TALE/KNOX homeobox family. CC -:- SIMILARITY: Contains 1 homeobox domain.
CO CO CO CO CO CO CO CO	Db 234 Sergin

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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMB. outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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POLY-ASN.
POLY-SER.
ASP/GLU-RICH (ACIDIC).
ELK DOMAIN.
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Matches:
Conservative:
Mismatches:
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HisProlleAsnProSerAsnAsnAsnAsn----
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InterPro; IPR00155; Homeobox.
InterPro; IPR00155; Homeobox.
InterPro; IPR005540; KNOX1.
InterPro; IPR005541; KNOX2.
Pfam, PP03789; ELK; 1.
Pfam, PP03799; KNOX1; 1.
Pfam, PP03791; KNOX2; 1.
ProDom; PD000010; Homeobox; 1.
SMMRT; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Nuclear protein; Txa
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42374 MW;
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HSSP; P41778; 1DU6.
TRANSFAC; T04052; -.
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379 AA;
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DOMAIN
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|||-
---LysValGlyAlaProProGluValValAlaArgLeuGluGluAlaCysAlaSerAla
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                                                                                                                 CTITCATIGAGICTIGCALCAGAIGITICIGAIGAAIGCICGGAGAIAAGICTITGIGCA
                                                                                                                                                                                                                                     ----TCTTGCAGCAGCAAGACATTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 GluAlaMetLeuPheLeuGlnArgIleGluCysGlnPheLysAsnLeuThr---IleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1054 GATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGGAGGAGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 SerSerAspPheAlaSerAsnGluGlyGly-----
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15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
LETG.
LETG.
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1036 AATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACA 1095
                                                                                                                                                                                                                                                                                                                                                      91 SerSerSerSerIleLysSerLysIleMetAlaHisProHisTyrHisArgLeuLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                       111 ThrAlaTyrLeuAsnCysGlnLysIleGlyAlaProProGluValValAlaArgLeuGlu 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                         865 GACATITCTAATAACGTIGTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATAC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 TyrdluglngluLeuSerLysProPheLysGluAlaMetValPheLeuSerArgIleGlu 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            976 TATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCACGTTTTGAG
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                                                                                                                  598 GATCATTTAAGACACTATGATGATTCCTCAAACAACATGTGGGGGTTTTGAAGCAAATAGT
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                                                                                                                                                                                                                                                                                    -----PheLeuProPheMetAspAsnAsnAsnAsnAsnAsnProGlnGluAspAsnAsn
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                                                                              ThrileCysAlaProProMetMetMetMetProProProProPro-
                                                                                                                                                 59 ThrasnasnasnalaGluThrSerasnasnasnIleLeu---
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||| ::: ::: 28 AsnAsnGlyAsnGlyAsn---
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                                                553 GAGTICAIGGCICCICT
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              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                 from tomato.";
Plant Mol. Biol. 36:417-425(1998).
-!- FUNCTION: May have a role to play in formative events in ovule and
-!- FUNCTION: May have a role to play in formative events in ovule and
-!- EUNCTION: May have a role to play in formative events in ovule and
                                                                                  [1] SEQUENCE FROM N.A.
STRAIN=cv. VFNT Cherry,
MEDLINE=98145476; PubMed=9484482;
MARDINE=98145476; PubMed=9.7., Mathern J., Hake S., Sinha N.;
"Isolation and characterization of two knotted-like homeobox genes
                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Nuclear (Probable).
-:- TISSUE SPECIFICITY: Expressed in developing lateral organs and developing ovaries in Flowers.
-:- SIMILARITY: Belongs to the TALE/KNOX homeobox family.
-:- SIMILARITY: Contains 1 homeobox domain.
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9E9A1AFD75808C49 C
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Matches:
Conservative:
Mismatches:
Indels:
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POLY-ASN
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POLY-MET,
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POLY-SER.
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R InterPro, IPR001356; Homeobox.
R InterPro; IPR001356; Homeobox.
R InterPro; IPR005541; KNOX2.
Pfam; PF03789; ELK; 1.
Pfam; PF03789; KNOX1; 1.
Pfam; PF03791; KNOX1; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX: 1.
Lycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
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PIR; T04317; T04317.
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39796 MW;
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Best Local Similarity:
                                                                  NCBI_TaxID=4081;
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-----CysGln 192

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-----Leulysgln

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RASIONENCE FROM N.A.

REPAGENCE FROM N.A.

REPAGENCE FROM N.A.

REPAGENCE FROM N.A.

REPAGENCE S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E., Kaneko T., Nakawashima K., Marzaki N., Marsumoto M., Muraki A., Nakayama S., Kaneko T., Marsumoto M., Muraki A., Nakayama S., Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T., Rahange E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R., Hadreman K., Muray J., Johnson D., Rohlfing T., Nelson J., Becker M., Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M., Rahermann K., Muray J., Johnson D., Rohlfing T., Nelson J., Rahermann S., Neyer R., Mulvaney E., Courtney W., Dante M., Cordes M., Courtney W., Dante M., Belter E., Cordum H., Cordes M., Courtney W., Dante M., Balter E., Latreille P., RA Benell E., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J., RA Magner-Merherson C., Wollam A., Yoakum M., Bell M., Dedhia N., RA Martienssen R., McCondiaw R., Wilson R.K., Mulphy G., Bancroft I., Shah R., McChillagh B., Robben J., Grymonprez B., Zimmermann W., RA Bentan G., Waduer H., Balke K., Wedler E., Deberes S., Hempel S., Rayansperger T., Bothe G., Rese M., Hauff J., Benneiser S., Hempel S., Reldpausen M., Landberth S., Villarroel R., Gielen J., Ardiles W., Reldpausen M., Lemberth S., Villarroel R., Gielen J., Ardiles W., Rayaneller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P., Rayaneller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P., Fransidopsis
                                         1573 ATAAATGCGCGGGTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAAC 1632
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291 GlnLysLeuAlaLeuAlaGluSerThrGlyLeuAspGlnLysGlnIleAsnAsnTrpPhe 310
                                                                           MEDLINE=97304677; PubMed=9161040;
Serikawa K.A., Martinez-Laborda A., Kim H.S., Zambryski P.C.;
"Localization of expression of KNAT3, a class 2 knotted1-like gene.";
Plant J. 11:853-861(1997)
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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-1- SIMILARITY: Belongs to the TALE/KNOX homeobox family.
-1- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
116-MAR-2004 (Rel. 43, Last annotation update)
NAR-3 OR ATSG25520 OR F2116.18.
Arabidopsis thaliana (Mouse-ear cress).
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TRANSFAC; T04044; -
InterPro; IPR005539; ELK.
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                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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958 GCCGCATACTCGCTCGATTATTCATCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCC 1017
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143 GlyGlyAlaThrAlaAlaAspGlyValValSerTrpGlnAsnAlaArgHisLysAla--- 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AsnThrAlaLeuLeuArgSerSerAspAsnAsnAsnAsnPheLeuAsnLeuHisThrAla 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ThrAlaAsnThrThrAlaSerSerSerAspSerProSerSerAlaAlaAlaAla 88
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POLY-PRO.
POLY-ARO.
POLY-ASN.
POLY-ASN.
POLY-ASN.
FIK DOWAIN.
HOMEOBOX (TALE-TYPE).
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InterPro; IPR001356; Homeobox.
InterPro; IPR005540; KNOX1.
InterPro; IPR005541; KNOX2.
InterPro; IPR005541; KNOX2.
Pfam; PF03790; KNOX2; 1.
ProDom; PD000010; Homeobox; 1.
PROSITE; PS000027; HOMEOBOX 2; 1.
PROSITE; PS000027; HOMEOBOX 2; 1.
PROSITE; PS000077; HOMEOBOX 2; 1.
HOMEOBOX: DNA-binding; Nuclear prot DOMAIN 34 37 POLY-IDOMAIN 34 37 POLY-IDOMAIN 104 108 POLY-IDOMAIN 32 34 BELK DOMAIN 320 343 ELK DOMAIN 320 343 ELK DOMAIN 34 4 406 HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOBOX 20077; HOMEOB
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FEBS Lett. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                1555 CAGGTATCAAACTGGTTTATAAATGCGGGGTTAGGCTATGGAAGCCGATGATAGAAGAG 1614
                                                      1138 GATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTT 1197
                                                                                                  1198 ATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTC 1257
             GCGGGTTTCGGATCTACATTTCAAAGGAGAGCATTAGAAGCAAAGAAACCCGATCTCTTG 1137
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270 SerProGlyGluGlyMetGlyAlaThrMetSerAspAspGluAspGluGlnValGluSer 289
                                                                                                                                                                                                                                                        310 GluSerGluArgSerLeuMetGluArgValArgGlnGluLeuLysHisGluLeuLysGin 329
                                                                                                                                                                                                                                                                                              350 LysLeuProGlyAspThrThrSerValLeuLysAlaTrpTrpGlnSerHisSerLysTrp 369
                                                                                                                                                                                                                                                                                                                                                                                    390 GinileAsnAsnTrpPheileAsnGlnArgLysArgAsnTrpHisSerAsnProSerSer 409
                                                                            232 LeuLeuLeuCysSerPheLysGluGlnLeuGlnGlnHisVal---ArgValHis---Ala 249
                                                                                                               212 AlaAlaGlnGlyLeuValGlyAspAspLysGluLeuAspGlnPheMetThrHisTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. C1; TISSUE=Leaf;
MUBDIRNE=9521651; PubMed=7715728;
Mueller K.J., Romano N., Gerstner O., Garcia-Maroto F., Pozzi C., Salamini F., Rohde W.;
The barley hooded mutation caused by a duplication in a homeobox open intron.";
Nature 374:727-730(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND IDENTIFICATION OF DNA-BINDING SITE. STRAIN=cv. Bomi; TISSUE=Seedling; MEDLINE=97324092; PubMed=9180261; Krusell L., Rasmussen I., Gausing K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1615 ATGTATGCGGAAATGAACAAGAGGAAGCTCAAT 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 SerThrValLeuLysAsnLysArgLysSerAsn 420
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Homeobox protein KNOX3 (Hooded protein).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   rebb bett, 40016273714371.

-I- FUNCTION: May play a role in meristem formation and/or maintenance. Overexpression causes the hooded phenotype characterized by the appearance of an extra flower of inverse characterized by the appearance of an extra flower of inverse polarity on the lemma. Binds to the DNA sequence 5'-TGAC-3'.

-I- SUBCELIULAR LOCATION: Nuclear (Probable).

-I- SUBCELIULAR LOCATION: Nuclear (Probable).

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"DNA binding sites recognised in vitro by a knotted class 1 homeodomain protein encoded by the hooded gene, k, in barley (Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression is down-regulated.
SIMILARITY: Belongs to the TALE/KNOX homeobox family.
SIMILARITY: Contains 1 homeobox domain.
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G -> V (IN REF. 2),
60999A1B3AB3EAAA CRC64;
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BRIS, S8871; S58871.
HSSP, P40474; 1B2.
TRANSFAC; T05583; --
TRANSFAC; T05583; --
TREPER, PF000539; ELK.
INTERPER, PR005135; HOMEODOX.
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PEAM; PF03789; ELK; 1.
PEAM; PF03789; ELK; 1.
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Q94K14 arabidopsis
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Q7y0z8 lycopersico
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Q7y0z9 lycopersico
Q84K12 arabidopsis
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Q81029 lycopersico
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Q85U8 mabidopsis
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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STRAIN=CV. Colombia, TISSUE-Rosette leaves;
STRAIN=CV. Colombia, TISSUE-Rosette leaves;
SUBCLINE-92210927; PubMed-769678;
Quaedvlieg N., Dockx J., Rook F., Weisbeek P., Smeekens S.;
The Homeobox gene ATH1 of Arabidopsis is depressed in the photomorphogenic mutants cop1 and det1.";
Plant Cell 7:117-126(1995).
EMBL; X80127; CAS124626.1; -.
SEQUENCE 469 AA; 53477 MW; 3DC7C6A976819574 CRC64;
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     NCBI_TaxID=3702;
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                          OM nucleic - protein search, using frame_plus_n2p model
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Xgapop 10.0, Xgapext
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### 19.96-208 Length: 469 ### 20.00 MacChes: 469 ### 20.153 Conservative: 0 ### 10.703 Conservative: 0 ### 20.153 Conservative: 0 ### 20.153 Index: 1 ### 20.153 In	Qy 1264 GTTTCCTTCTTATACAAGAACCTGAAGAATCTCGCAAGAAGATAATCTCTATGGGA 1323 Db 317 ValSerbheLeuTyrLksAsnLeuArgGluArgGlaCysLysLleIleSerMetGly 336 Qy 1324 TCTGTATTGGAAGAGAGAAGACTCAAGAACCTCTATGTTCCACCAGCATTGC 1383 Db 337 SerValLeuGluArgGlyLysAspLysThrGlnGluThrSerMetPheHisGlnHisCys 356 Qy 1384 CTTCTTCAGCAGAAGAACGAAAGAACCATCAGATTTGGAGACCTCAACGTGCTTGC 1443 Db 357 LeuLeuGlnGlnLeuLysAspLysThrGlnGlnTHTSerMetPheHisGlnHisCys 356 Db 357 LeuLeuGlnGlnLeuLysAspLysThrGlnGlnTeTrpArgProGlnArgGlyLeuPro 376	CAAAACTTCCTTCACCCTTACCCG 1	Oy 1624 GAATGAAGGAAGCTGAATAACAGTCACATTGAACCAACGGACCAACTTTCGA 1683	1 5	Trui, Magnostophyra, Charlocytechnis, Core Courtocy, Accordances, Solanum. 4081, ROM N.A. rnis A., Lifschitz E.; Rimx-2001) to the EMBL/GenBank/DDBJ databases. 5967, AAP470c6.1; 597 Homeobox; Nuclear protein. 323 AA; 37216 MW; DED2C654B526D6F1 CRC64;	Alignment Scores: 3.37e-56 Length: 323 Score: 736.50 Matches: 166 Score: Similarity: 65.16% Conservative: 36 Best Local Similarity: 53.55% Mismatches: 72 Query Match: 10 Gaps: 7 US-09-423-575-1 (1-1886) x QYVOZ6 (1-323)	Qy 793 GATGAATGCTCGGAGATAAGTCTTTGTGCAGCTACA
0	Scores: 9.9e-208	AATCCTCTTCTCATGGATTTTATACCTTCAAGAGAAGATTCAACTTCATCTCTCAACAATG 42	CGCAATGTTGAGTTCATGGCTCCTCCTCCTCCTCCTCCTCCTCTCTTTTGGATCAT 60	GATTICCGGTTTCTAATTTCGAATAAAGAAACAATGAGCTTTCATTGATTG	* CAAGCTTCTTGCAGCAACAACATTCTAATAACGTTGTTACTCAAGGTTTCTCTCAA 9	217 TyrserleuaspTyrserSerArgGiyThrGiuSerGiyalaAlaserserAlaPheThr 236 024 TCACGTTTTGAGAATATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGT 108 024 TCACGTTTTGAAATAACTGAGTTTCTTGATGGTGATTCTAATAACTCGGAGGCGGGT 108 025 SerArgPheGluasnileThrGluPheLeuaspGlyaspSerAsnAsnSerGluAlaGly 256 084 TTCGGATCTACATTTCAAAGGAGAGCATTAGAAGCAAAAAAAA	144 CTTCAAAIGGTGGATGATAGTCATTGCGTAGATGAGATTCATACGGTTATATCA [

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OY 883 GTTACTCAAGGTTTCTCTCAACTTATATTTGGCTCAAAATACCTTCACTCTGTTCAAGAA 942	ACTATCTCATTTCGCCGCATACTCGCTCGATTATTCATCT	Qy 985 CGAGGAACCGAGTCAGGCTGCTAGTTCAGCCTTTACTTCACGATTTTGAGAATATAACT 1044 Db 82 AsnGlyThrGluAsnGlyAlaAsnThrSer 91	Qy 1045 GAGTTTCTTGATGATTCTAATAACTCGGAGGCGGGTTTCGGATCTACATTTCAAAGG 1104	QY 1105 AGAGCATTAGAAGCAAAAACCCATCTCTTGGATCTTCTTCAAATGGTG 1155	Oy 1156 GATGATGGTATAGGCTAGAGATTCATAGGTTATATCAGGGTTCCATGCT 1215	OY 1216 GCAACCGAGTTAGATCCACAGTTACACACCCGGTTTGCCCTCCAAACCGTTTCCTTCTTA 1275	Qy 1276 TACAAGAACCTGAGAGA-GAGAAICTGCAAGAAGATAATCTCTATGGGATCTGTATTGGA 1334	Qy 1335 GAGAGGCAAAGACAAGACTCAAGAAACCTCTATGTTCCACCACATTGCCTT 1386 ::: ::: :::	Qy 1387CTTCAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGCCCTCAACGAGG 1436	Qy 1437 TTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTTGGATGTTCCAAACCTTCCTT	OY 1497 TTACCGGAAGGTTCGGAGAACGTCTTCTAGCTATACGAAGTGGCTTGACAAGAGTCA 1556	Qy 1557 GGTATCAAACTGGTTTATAAATGCGGGGTTTAGGGCTTAGGAAGCCGATGATAGAAGAGAT 1616 	Oy 1617 GTATGCGGAAATGAACAAGAGGAAGCTC 1644	RESULT 3 27YOZ7 ID Q7YOZ7 PRELIMINARY; PRT, 699 AA.	AC Q7Y0Z7, DT 01-OCT-2003 (TrEMBLrel. 25, Created) DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE Bell-like homeodomain protein 2.	N BLS. Lycopersicon esculentum (Tomato). Divopersicon esculentum (Tomato). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; lamiids: Solanales: Solanacese: Solanacese: Solanam.	XX NCBI_TaxID=4081; NN [1] NN [1] NP SEQUENCE FROM N.A.
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220 LeulysAlaAlaGlnGluLeuLeuAspGlu---ValValAsnIleValGlyLysSerAsn 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 AACACTTTTAGTTCTCTGGATAATGTCATGACT-----AACCAAAATCCTCTT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 CTCATGGATTTTATACCTTCAAGAGATTCAACTTCATTCTCAACAATGCTTCCATGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 AATACCATCAGATCAGATCCTCTACAAATGGGTGGCTTTGATATTTTCAATTCTATGCTG 492
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| 134 AlaThrSerCysGlyGlyThrThrAspLeuAlaSerGlnLeuAlaPheGlnArgPro 153
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154 IleValValSerProThrProGlnHisArgGlnGlnGlnGlnGlnGlnGlnGlyGlyLeuSer 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925 CTICACICIGIICAAGAAAIACIAICICAIIITGGCGGCAIACICGCICGAITAIICAICT 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 ACATTCGGT-----CAAGAAGATTTC-------CCG 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AsnLeuGlyAsnSerAsnAsnAsnIleGlnThrLeuTyrLeuMetAsnProAsnSerTyr 41
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Ron N., Parnis A., Lifschitz E.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR375966; AAP47025.1; -
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 699 AA; 77662 MW; 535A17C9D5A68362 CRC64;
                                                                                                                                                                         699
152
87
169
120
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                          9-423-575-1 (1-1886) x Q7Y0Z7 (1-699)
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487.00
45.278
28.79%
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DR GO; GO:0005634; C:nucleus; IEA. DR GO; GO:0003700; F:transcription factor activity; IEA. DR. GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. DR InterPro; IPR001556; Homeobox. DR Ffam; PF00046; homeobox; 1. DR PROD; BD000100; homeobox; 1. DR SMART; SM00399; HOX; 1. DR SMART; SM00574; POX; 1. DR PROS;TE; PS00027; HOMEOBOX 1; 1. DR SGO171; HOMEOBOX 1; 1. DR SGO171; HOMEOBOX 1; 1. SQ SEQUENCE 688 AA; 76459 \M; 4451807DDF525781 CRC64;	Alignment Scores: 3.37e-33 Length: 688 Pred. No.: 3.47.00 Matches: 150 Score: 477.00 Conservative: 89 Best Local Similarity: 28.63\$ Mismatches: 170 Query Match: 10.2863\$ Indels: 18 US-09-423-575-1 (1-1886) x QBLLE4 (1-688)	Oy 264 TTCTATCAGAAGAAGAATAAAGTTTCATAGAAACCCAATGGACAACAACAACAA 323	372	Qy 432 GAATACCATCAGATCAGATCCTCTACAAATGGGTGGCTTTGATATTTCAATTCTATGCT 491	Qy 492 GACTAACAAATACTTATCATCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGT 551 .::	Oy 552 TGAG	Qy 588 TCATCCTTTGGATCATTAAGACACTATGATGATCCTCAAACATGTGGGGTTTTGA 647	Oy 648 AGCAAATAGTGAGTTTCAGGCATTTTCAGGTGTAGTGGTCCAAGTGAACCAATGATGTC 707	::::: ::::	Oy 754	Qy 777 IGCATCAGAIGTITCTGATGAATGCTCGGAGATAAGTCTITGIGCAGCTAC 827	828 AAGAITAGCCTCAGAGCAAGCITCTIGCAGCAAGGAAGACATTTCTAATAACGTIGITAC 	888 TCAAGGTTTCTCTCAACTTATTTGGCTCAAATACCTTCACTC 9
	Db 296 LysAlaLysLeuLeudludluValGluGlnArgTyrArgGlnTyrHisHis 315 Qy 1183 GAGATTCATAGGTTATAATCAGGTTCCATGCTCCAACCGAGTTAGATCCACĀĞTTA 1239 Db 316 GlnMetGlnIleIValSerSerPheGluGlnValAlaGlyValGlySerAlaLysSer 335 Qy 1240 CACACCCGGTTTGCCCTCCAACCGTTTCCTTCTTATAACAAGAAGAAGAAGAAGAATC 1299 ::: :::: :::: ::::	Oy 1300 TGCAAGAAGATAATCTCT	1390 CAGCAGCTGAAAGGAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAA 395 GlnGlnLeuGlyMetMetGlnProAenAlaTrpArgProGlnArgGlyLeuProGluArg	OY 1450 TCTGTTTCGGTTCTACGGAATTGGATGTTCCAAAACTTCCTTC	OY 1510 TCGCAGAAACATCTTCTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAAACTGG 1569	OY 1570 TITATAAATGCGCGGGTTAGGCTATGGAGCCGATGATAGAAGATGTATGCGGAAATG 1629	Qy 1630 AACAAGAGGTCAATAACAGT 1653 Qy 1630 AACAAGAAGGTCAATAACAGT 1653 Db 475 ValLysAsnGlnGluGlnAsnSer 482	SULT 4 LLE4 QBLLE4 QBLLE4; 01-OCT-2002	DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DB BEL1-related homeotic protein 5.	BELS. Solanum tuberosum (Potato). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,	Spermatophyta; Magnollophyta; eudloofyledons; core eu lamiids; Solanales; Solanaceae; Solanum. NCBL_TaxID=4113;		family of transcription factors."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF406697; AAN03621.1;

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283 ATAAAGITICATAGAAACCCCAATGGACAACAACAACAACAACAACACTITITAGITCTCTG 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AsnAsnAsnThrAsnThrAsnAsnAsnAsnAsnSerSerPheValPheLeuAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGAAGATTCAACTTCTTCAACAATGCTTCCATGGAATACCATCAGATCAGATCCT
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GlnGlnGlnGlnGlnHisHisHisGlnHisGlnProlleHisValGlyPheGlySer
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                                                                                            Latinited (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R GO, GO:0005634; AAK43836.1; -..

R GO, GO:0005634; Cinucleus; IEA.

R GO; GO:0005635; Cinucleus; IEA.

R GO; GO:0003700; Fitramscription factor activity; IEA.

R DITERPRO; IPRO01356; Homeobox.

R InterPro; IPRO06563; Pox.

R ProDom; PRO0046; homeobox; 1.

R ProDom; PRO0059; Howeobox; 1.

R SMART; SM0059; HOX; 1.

R RACSITE; PS00027; HOMEOBOX 1; 1.

R PROSITE; PS00027; HOMEOBOX 1; 1.

R PROSITE; PS00011; HOMEOBOX 2; 1.

R PADSITE; PS00014; HOMEOBOX 2; 1.

R PADSITE; PS00014; HOMEOBOX 2; 1.

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SEQUENCE FROM N.A.
Pidkowich M.S., Samach A., Modrusan Z., Haughn G.W.;
"A family of BEL1-like homeodomain (BLH) proteins in Arabidopsis
thaliana.";
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152
74
1193
1119
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Matches:
Conservative:
Mismatches:
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1126 ACCCATCTCTTGTACATTGTGCTGCATGATCGATATAGTCGATATAGTCATTGCGTAGATGAG 1185
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                                                                                                                                                  213 AspMetAsnAlaLysSerGlnLeuPheSerSerLysLysGlySerCysGlyAsnAspLys 232
                                                                                                                                                                                                                       233 ProValGlyGluSerSerAlaGlyAlaGlyGlyGluGlySerGlyGlyBlaGluAla 252
                                                                                                                                                                                                                                                                                                                                                                                                              273 AlalysLeuSerAsnMetLeuHisGluValGluGlnArgTyrArgGlnTyrHisGlnGln 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 SerValSerGlyValGlyArgPheGluGlySerArgLeuLysPheValAspHisHisLeu 366
                         GluLysThrProLeuAspGlnSerAsnGluAspSerAlaSerLysSerThrSerAsnGln
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                                                                                                                                                                                           1051 CTTGATGGTGATTCTAATAACTCGGAGGCGGGTTTCGGATCT---
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Putative homeodomain transcription factor (At2g35940).
                                                           199 AlaGluceuLeuAspGluValValAsnAlaAspSerAsp
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Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AV07175; AALS9971; --
EMBL, AY09654; AAM201981; --
EMBL, AY09654, AAM201051; --
EMBL, BY008422; AAR207051.; --
                                                                                                                                                                                                                                                                                         STRAINTECT COlumbia; MRDLINES COLUMBIAS, S. S. STRAINTECT COLUMBIAS, S. S. School S. D., Shea T.P., Benito M.-I., Town C.D., Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo. H., Mcffat K.S., Cronin L.A., Shen M., Vanken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
Palm C.J., Bowser I., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

Yamada K., Banh J., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones

Kamiya A., Karlinn Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki Javis R.W., Ecker J.R., Theologis A.,

"Full Length cDNA of gene Aleg35940 (GI:15227535).",

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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213 1051 233 1093 253	. 273 1186 293 1243 313	1303 333 1363 347	1387 367 1423 387 1483	1543 1543 1603 1427 1447	17 2811 2811 2811 2011 2011 3811 3811 3811 4681 4681 4681
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IEA.		TCTCTG 342 SerAsn 51 CCTTCA 393 ABDSer 71	GATCCT 45 87 TCATCT 51 A S 90	CTCCTCCT 573 CAAACAAC 633 hrHisGln 126 GTCCAAGT 693	GAGATAAAGA 753 YPheGlySer 166 GGAGATAAGT 813
factor activity; IEA. transcription, DNA-dependent; rotein.	Length: 680 Matches: 152 Conservative: 74 Mismatches: 193 Indels: 119 Gaps: 13	1 (1-1886) X CYSUSE (1-880) ATAAAGTTTCATAGAACACAACAACAACAACAACAACAACATTTAGTTCT **********************************	AGAGAAGATTCAACTTCTCAACAATGCTTCCATGGAATACCATCAGATCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	TCTCCACGGTCTATCGATGTTCAAGATAACCGCAATGTTGAGTTCATGGCTCCTCCTCCTCTTG1AlaAlaAspAsn11eserValLeuHisG1yTyrProProArgCTCTCCTCCTCCTCTCTCATCATTTAAASPASN11eserValLeuHisG1yTyrProProArgCATCCTCCACTTCATCATTTGAACACTATTAAACAATATTTAAACAACATATTAAACAACA	CTAATTTC HISTORY GAATGCTC AGCAGCAA TCAAAATA TATTCATC TATTCAT
PIR; H84774; H84774. HSSP; P01366; LAKH. GO; GO:0003503; C:nucleus; IEA. GO; GO:0003700; F:transcription GO; GO:000355; P:regulation of InterPro; IPR001356; Homeobox; Prom; PF000046; homeobox; PROSITE; PS00027; HOMEOBOX; I. PROSITE; PS00027; HOMEOBOX; I. PROSITE; PS00027; HOMEOBOX; I. PROBLITE; PS00027; HOMEOBOX; I. PROBLITE; PS00027; HOMEOBOX; I. SEQUENCE (800 AA); 74463 MW); 4,	int Scores: 9.288-33 472.00 5.Similarity: 42.01% ocal Similarity: 14.37%	283 ATAAAGTTTCATAGAAACCCAATGGACAACAACAACAACAACAAAAGTTTCATAGAAACCCCAATGGACAACAACAACAACAAAAAAAA	A H D · E	514 TCTCCACGTCTATCGATGTTCA	694 GAACCAATGATGTACATTCGGTGAAGAAGATTTCCCGTTT 117 117 118 118 118 118 118 118 118 118
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COCTATATATCAGGGTTCCATGCTGCAACCGAGTTA- SUVALIISESESEPHGGIUGINALAALAGJYIIGG TTGCCCTCCAAACGTTTCTTATACAAGAACG TTGCCCTCCAAACGTTTCTTATACAAGAACG TTGCCCTCCAAACGTTTCTTATACAAGAACGCAAAG TAATCTCTATGGGATCTGTATTGGAGAGGCAAAG TTGCTCTATGGGATCTGTATTGGAGAGGCAAAG TTGCTCTATGGGATCTGTATTGGAGAGGCAAAG TTGCTCTATGGGATCTGTATTGGAGAAGGAAACGAAAGGAAAGGTTTGCCTGAAACGAAAGGAAACTGTTTCGGTTCTACTACAGAAACGAAACTGTTTCGGTTCTACTACAGAAACACAAACAGAAACGGGGGGGG
TATCTCTATGGGATCTGTATTGGAGAGAGGGAAGAGAGGCAAGAGGGAAGAGGGAGGGGGG
"Argala Leudinginieudiymetiledinitisprosi Accadgartrigactagaaaattrotritagaluarga, Targaly Leu Prodiuargalaval Serval Leu Arga, Targaly Leu Prodiuargalaval Serval Leu Arga, Targaly Leu Prodiuarga Argana
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CGGAATTGGATGTTCCAAAACTTCCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTT 1524
                                                                                                     1525 CTAGCTATACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGG 1584
                                                                                                                                                                        GTTAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTC 1644
                                                                                                                                                                                          823 GCTACAAGATTA---GCCTCAGAGCAAGCTTCTTGCAGCAACAAAGACATT---TCTAAT 876
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237 MetGlnThrasnAlaTrpLysProGlnArgGlyLeuProGluArgAlaValSerValLeu 256
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTCATTGAGTCTTGCATCAGATGTTTCTGATGAATGCTCGGAGATAAGTCTTTGTGCA
                                                       TRAIN-CV. Desiree;
Chen H., Rosin F.M., Hannapel D.J.;
Chen H., Rosin F.M., Hannapel D.J.;
A KNOX protein of potato interacts with several members of the TALE
family of transcription factors.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF406702; AAN03626.1;
GO, GO:0003700; F: transcription factor activity; IEA.
GO; GO:0003700; F: transcription of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR006563; POX.
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                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
BELL-related homeotic protein 29 (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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ProDom; PD00010; Homeobox; 1.
SWART; SM00389; HOX; 1.
SWART; SM00574; POX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
SRQÜENCE 567 AA; 62770 MW; 4B3
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55.06%
37.97%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          976 TATICA----TCTCGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTTACTTCACGTTTT 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .138 GATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTT 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1198 ATATCAGCGTTCCATGCTGCAACCGAGTTA---GATCCACAGTTACACACCCGGTTTGCC 1254
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218 LeuLysPheValAspHisHisLeuArgGlnGlnArgAla---LeuGlnGlnLeuGlyMet 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 856 AGCAGCAAAGACATTTCTAATAACGTTGTTACTCAAGGTTTCTCTCAACTTATATTTGGC 915
                  CTRAINSCY. Desiree;

A Chen H., Rosin F.M., Hannapel D.J.;

CHEN H., Rosin F.M., Hannapel D.J.;

CHEN H., Rosin F.M., Hannapel D.J.;

Tamily of transcription factors.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

I. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

BEL; AR40668; AAN03622.1;

R GO; GO:0003634; C:nucleus; I.F.

R O; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

R INTERPO: IPR001356; Homeobox.

R INTERPO: IPR00146; Homeobox; 1.

R Prodom; PD000010; Homeobox; 1.

R PROSITE; PS00027; HOMEOBOX_1; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.
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------MetIleLeuGly
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Conservative:
Mismatches:
Indels:
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   SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                              HisAspValAsnHisSerArgHisLeuMetAspLeuLeuGlyAlaSerHisAspAlaAsn
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|ThrPheThrAsnAsn-----ProSerTyrMetAsnGlnGluIleAspGlnArgAsnAsn
                                                                                                                                                                                                           TITGATATITICAATICTATGCTGACTAACAAATACTTATCATCTTCTCCACGGTCTATC
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| CysGlyThrGluSerPheValSerAlaileGlyAsnSerLysTyrLeuLysProThrGln
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Matches:
Conservative:
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                    protein
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    EMBL; AF375965; AAP47024.1; -. DNA-binding; Homeobox; Nuclear
                                            AA; 44877 MW;
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                                                                                  6.38e-31
450.50
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Best Local Similarity:
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GlnGlnGlnGlnSerIleSerSerValProLeuSerSerLysTyrMetLysAlaala
                                      CAAGAAATACTATCTCATTTCGCCGCATACTCGCTCGATTATTCATCTCGAGGAACCGAG
                                                        ||||||:::|||
|GlnGluLeuLeuLeuAspGlu-----ValValAsnValGlyLysSerMetLysSerThrAsn
                                                                                         TCA----GGAGCTGCTAGTTCAGCCTTTACTTCACGTTTTGAGAATATAACTGAGTTT---
                                                                                                                                                ----CTTGATGGT-----GATTCTAATAACTCGGAGGCGGGTTTCGGATCTACA
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|SerThrAspValValValAsnAspValLysLysSerLysAsnMetGlyAspMetAsp
                                                                                                                                                                                                                      Lycopersicon esculentum (Tomato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                  TTATACAAGAACCTGAGAGAGAATCTGCAAGAAGATA---------
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Bell-like homeodomain protein 1 (Fragment).
BLI.
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                                         1371
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                                                                                                                                                       ::: ||| | ::: ||| GluLysGluThrLeuGlnAsnArgIleSerLeuGlnGlnLeuGlyIleIleGlnSerAsn 297
                                                                                                                                                                                                                                    298 ArgGlnAlaTrpGlnProlleArgGlyLeuProGluThrSerValAlaPheLeuArgSer 317
                                                                                                                                                                                                                                                                                                                     SerGlnThrGlyLeuSerLygAsnGlnValSerAsnTrpPhelleAsnAlaArgValArg 357
MetSerArgHisPheCysCysLeuArgAspSerIleIleSerGlnIleAsnPheIleArg 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum (Potato).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Manoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                          1372 CACCAGCATTGCCTT----CTTCAGCAGCTGAAA-----CGAAAGAAC
                                         -- ACTCAAGAAACCTCTATGTTC
                                                                              GlnLysMetProArgAspValProLysIleSerSerGlyLeuSerHisLeuSerLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the TALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINCY. Desiree,
Chen H., Rosin F.M., Hannapel D.J.;
A RNOX protein of potato interacts with several members of the TA family of transcription factors.';
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR406700; AAN03624.1;
GO; GO:0003503; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003505; P:requiation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; POX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S494C0BF29B18474 CRC64;
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132
61
123
123
17
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 24, Last annotation update)
BELL-related homeotic protein 14 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTATGGAAGCCGATGATAGAAGAGATGTATGCGGAA 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 LeuTrpLysProMetileGluGluMetTyrLysGlu 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532 AA
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Matches:
                                           1324 TCTGTATTGGAGAGAGGCAAAGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-423-575-1 (1-1886) x Q8LLE1 (1-532)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PF00046; homeobox; 1.
ProDom; PD00010; Homeobox; 1.
SWART; SM0389; HOX; 1.
SWART; SM00574; POX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 AA; 59757 MW;
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450.50
46.51%
31.81%
13.72%
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SEQUENCE
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DB:
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QUELE AC QUELE AC QUELE AC QUELE DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT O1-OCD DT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----CGAGGAACCGAGTCAGGAGCTGCTAGTTCAGCCTTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1021 ACTICACGITITIGAGAATAIAACTGAGITICTTGATGGTGATICTAATAACTCGGAGGCG 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928 CACTCTGTTCAAGAAATACTATCTCATTTCGCCGCATACTCGCTC------GAT 975
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ThrLysMetAlaMetGlyGlu-------TysAspSerThrSerThrLeuIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 ProGlySerThrArgGlyĠluThrProArgLeuArgLeuLeuAspGlnThrLeuArgĠln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  790 TCTGATGATGCTCGGAGATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081 GGTTTCGGATCTACATTTCAAAGGAGGAGTTAGAAGCAAAGAAAACCCATCTTGGAT
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                                                                                                                         570 ITTTCAGGTGTAGTTGGTCCAAGTGAACCAATGATGTCTACATTCGGTGAAGAAGATTTC
                                                                                                                                                                                                                                                                                                                  730 CCGTTTCTAATTTCGAATAAAAGAAACAATGAGCTTTCATTGAGTCTTGCATCAGATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                          59 ProcysGluGlyAsnGluArgProSerHisGlyLeuSerLeuSerLeuCys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           950 TCTTGCAGCAACAAGACATTTCTAATAACGTTGTTACTCAAGGTTTC-----
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                                                                                                                                                                                                                                --AspAspProSerMetArgCysVal--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 SerSerAsnProSerSerileGlyLeu--
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Best Local Similarity: 29.26\$ Mismatches: 170 Query Match: 13.52\$ Indels: 150 DB: 10 Gaps: 21 US-09-423-575-1 (1-1886) x Q9FWS9 (1-524)	OY 303 AATGGACAACAACAACAACATTTTAGTTCTCTGGAT	Qy 346AATGTCATGACTAACCAAAATCCTCTTCTGATGGATTTTATACCTTC 392	CTTCCATGGAATACCATCAGATCAGATCC : : : : : : :	OY 453 TCTACAAATGGGTGGCTTTGATTTTTCAATTCTATGCTGACTAACAATACTT 506		Qy 567 ICCICCICATCCTCCACTTCATCCTTTGGATCATTTAAGACACTATGATGATTCCTC 626		QY 687 TCCAAGTGAACCAATGATGTCTACATTCGGTGAAGAATTTCCCGTTTCTAATTTCGAA 746 Db 117	TAAAAGAAACAAIGAGCITTCATIGAGICTIGCAICAGAIGTITCIGAIGAAIGCICGGA 80	QY 807 GATAAGTCTTTGTGCAGCTACAAGATTAGCCTCAGAGCAAGCTTCTTGCAGCAAGAA 866 Db 139 OSErSerValTyrashas 145	Qy 867 CATITCTAATAACGTIGTT CATITCTC 899 145 145 146 146 146	95	Oy 960 CGCATACTCGCTCGATTATTCATCTCGAGGAACCGA 995	QY 996 GTCAGGAGCTGCTACTTCACGTTTTGAGAATATAACTGAGTTTCTTGA 1055	OY 1056 IGGTGATTCTAATAACTCGGAGCGGGTTTCGGATCTACATTCAAAGGAGAGCATTAGA 1115	QY 1116 AGGAAAGAAAACCCATCTCTGGATCTTCTTCAAATGGTGGATGATGGATG	Oy 1176 CGTAGATGAGATTCATACGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCC 1232 Db 254 rHisHisGlümlaLeualaSerSerPheGlümetValThrGlyLeuGlyalaAl 274
Db 343 ValSerAsnTrpPheileAsnAlaArgValArgLeuTrpLysProMetValGluGluMet 362 Qy 1618 TATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGACCAACT 1677	Qy 1678 CTTCGAATGCCAAATCTGTTATGATGACCAAGCAATGCATAAA 1722 ::::::: ::: 379SerLysAlaLeuIleAspAspMetThrIleHisGln 390	D 3	Ol. MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-WON-2003 (TrEMBLrel. 24, Last annotation update) F1B16.6 Drotein (F1B1.1) ike homeodomain nootain	pucative). FIB16.6 OR BLH3. Arabidopsis thaliana (Mouse-ear cress). Fivernorty of the contraction of the con	o buratyous, virialpiantes, Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis. ON NCBI_TAXID=3702;		KA BUGHLEr E., Chao Q., Chin C., Chiou J., Choi B., Gonzalez A., RA Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W., B. Suhmitted (conjoco)			RP SEQUENCE FROM N.A. RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; RT "Full-length messenger RNA sequences greatly improve genome RT annotarion ".	Genome Biol. 0:0-0(2002). [4] SEQUENCE FROM N.A.	RA Brover V., Iroukhan M., Alexandrov N., Lu YP., Flavell R., RA Feldmann K.; RT "Full-Length cDNA from Arabidopsis thaliana."; R Submitted (MRR-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL: ACO27754 AAG1305 1.	DR EMBL; AF353093; AAK43835.1; DR EMBL; AY085278; AAM62510.1; DR PIR; P96748; F96784. DR PIR; P96749; F96784.	DR GO, GO:0005634, C:nucleus, IEA. DR GO, GO:0003700, F:transcription factor activity, IEA. DR GO, GO:0006355, F:regulation of transcription, DNA-dependent, IEA. DR InterPro, IPR001356, Homeobox.	DR Pfam; PF00046; homeobox; 1. DR ProDom; PD000010; Homeobox; 1. DR PROSITE; PS00027; HOMEOBOX_1; 1. DR PROSITE; PS50071; HOMEOBOX_2; 1.	E E	

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-----AsnGlyLysSerLeuSerValHisGlnHisHisSerAspGlnIleLeuPr 139
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nasnGlyAsnAsnAsnAshArTyrAsnAsnTyrArgTyrGluThrSerGlyPheVa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 AAGAGAATTCAACTTCTTCAACAATGCTTCCATGGAATACCATCAGATCAGATCC 452
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Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
B. Ecker J., Theologis A., Davis R.W.;
W. Lubmitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY062545; AAL32623.1; -.,
R. GO, GO:000534; Criucleus; F.K.
R. GO, GO:000534; Criucleus; F.K.
R. GO, GO:000535; P:transcription of transcription, DNA-dependent; IEA.
R. GO; GO:000535; P:transcription of transcription, DNA-dependent; IEA.
R. TICEPTO; IPR00136; Homeobox.
R. R. PEDDOM: PD000010; Homeobox; 1.
R. SNART; SM00389; HOX; 1.
R. SNART; SM00389; HOX; 1.
R. SNART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOWEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 524 AA; 59693 NW; C9108DF9389A728E CRC64;
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                                                ACAGTIACACACCCGGITIGCCCTCCAAACCGITICCTTCTTATACAAGAACCTGAGAGA 1292
                                                                                                                                             GAGAATCTGCAAGAAGATA---ATCTCTATGGGATCTGTATTGGAGAGAGAGCAAAGACAA 1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SOUTDWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Soutbwick A., Karlin-Neumann G., Nguyen M., Lam B., Carninci P., Chen H.,
Carlin C.J., Bowser L., Jones T., Bah J., Carninci P., Chen H.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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ATIG75410, FIB16.6 OR ATIG75410.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Erreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
Nguyen M., Karlin-Neumann G., Banh J., Carninol P., Chen H.,
Palm C.J., Bowser L., Jones T., Banh J., Carninol P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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|ThrHisSerSerAlaGlnIleGluPheGlyLeuLeuAsnAsnHisAsnSerMetSerVal
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SEQUENCE FROM N.A.

STRAIMS—CV. Nipponbare;

Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,

Zismann C.Y., Yuan Q., Bowman C.L., Fujii C.Y., VanAken S.E.,

Zismann C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBa0003623 genomic sequence.";

Submitted (Aug-2010) to the EMBL/GenBank/DDBJ databases.

EMBL; AC079736; AAK00972.1;

FISSP; P41778; IDU6.
                                                                                                                                             Tracheophyta;
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G0; G0:0005634; C:nucleus; IEA.

G0; G0:0005634; C:nucleus; IEA.

G0; G0:0005536; P:transcription factor activity; IEA.

G0; G0:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR001356; Homeobox.

InterPro; IPR005631; POX.

Pfam; PF00046; homeobox; 1.

ProDom; PD000010; Homeobox; 1.
                                                                                         OSJNBAO003023.5.
OSJNBAO003023.5.
Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Trachs
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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PROSITE; PS00011; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nordlear protein.
SEQUENCE 642 AA; 71056 MW; 28322897B3371589 CRC64;
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134
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146
146
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative homeodomain protein.
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
DB:
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185 lSerValArgLysAspLeuLysLeuClyAsnLysLysMetLysAsnAspLysClyGlnAs
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       Lycopersicon esculentum (Tomato).

Eukaryota, Viridiplantee, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
lamids, Solanales, Solanaceae, Solanum.
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Matches:
Conservative:
Mismatches:
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                                                                                                              Ron N., Parnis A., Lifschitz E.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
Bubl; AF375964; AB47023.1; --
DNA-binding; Homeobox; Nuclear protein.
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LysGlnLeuLeuGlnSerLeuAsp-----
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436.00
45.14%
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PheArgCysLeuLysAspAlalleAsnAspGlnIleAsnVallleArgLysLysLeuGly 343
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344 GluGluSerSerSerGlyLysGluGlyLysLeuThrArgLeuArgTyrIleAspGln 363
                                244 GlyValSerSerAsnProGlnGluSerThrAlaAsnAlaAlaProGluIleSerAlaAla 263
                                                                       -----AsnAlaTrpArgProGlnArgGlyLeuProGluAsnSerValSerIleLeuArg
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                                                                                                   199 TyrLeuLysAlaAlaGlnGluLeuLeuAspGluValValSerValTrpLysSerIleLys
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Bell-like homeodomain protein 3 (Fragment).
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8.11e-29 427.50 44.09% 27.96% 13.02%

Percent Similarity: Best Local Similarity:

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      TCTATGTTCCACCAGCATTGCCTTCTT 1389
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                                                                                                               CAGCAGCTGAAACGAAAGAACCATCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAA
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|GlnGlnMetAsnMetMetGluThrHisProTrpArgProGlnArgGlyLeuProGluArg
                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MUELLEY. Bonus; Mueller J., Wang Y., Franzen R., Santi L., Salamini F., Rohde W.; Miterractions between barley TALE homeodomain proteins suggest a role for protein-protein associations in the regulation of Knox gene function.;
                                             245 ArgGlyGluThrProArgLeuArgLeuLeuAspGlnThrLeuArgGlnGlnLysAlaPhe
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
JUBEL1.
Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBL TRAID=4513;
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BMBL; AR334758; AR43845.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; R:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR006563; POX.
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ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
SMART; SM00574; POX; 1.
PROSITE; PS50017; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
SEQUENCE 759 AA; 80092 Mw; 982CE4AB3F4EA2A0 CRC64;
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Search completed: September 2, 2004, 12:11:44 Job time : 143 secs

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OM nucleic - nucleic	c search, using sw model	
Run on: Sept	<pre>September 2, 2004, 05:19:27 ; Search time 4991 Seconds (without alignments) 11284.326 Million cell updates/sec</pre>	
Title: US-09 Perfect score: 1886 Sequence: 1 att	US-09-423-575-1 1886 1 atttagttataaaaatgttgcttaaaaaaaaaaaa	
Scoring table: IDEN Gapo	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched: 2751	27513289 seqs, 14931090276 residues	
Total number of hits	s satisfying chosen parameters: 55026578	
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Post-processing: Min Max Lis	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
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CA917399 EST641546
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BE033022 Occ1510.
BE0331426 Occ1910.24.
BU011811 QG4117024.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AWOO44 LOCUS DEFINI ACCESS VERSIOS SOURCE SOURCE AUTH TITL JOURS COMMEN		AW004482 511 bp mRNA linear EST 08-SEP-1999	701931784 A. thaliana, mi	701931784, mRNA sequence.	~	N AW004482,1 GI:5851511	DS EST.	Arabidopsis thaliana (thale cress)		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,	Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,	<pre>Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,</pre>	<pre>Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,</pre>	Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and	Hanson, D.	E Arabidopsis thaliana Gene Expression MicroArray			Genome Systems, Inc., a wholly owned subsidiary of Incyte	Pharmaceuticals, Inc.	4633 World Parkway Circle, St. Louis, MO 63134, USA
	AW004482/C	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		-		REFERENCE	AUTHORS							TITLE	JOURNAL	COMMENT			

AW004482 701531784 AW004482 701557547 AV808362 AV808362 CB261894 83-E8862-

DB ID 9 AW004482 9 AI999808 9 AV808362 14 CB261894

Result Coore Match Length DB No. Score Match Length DB C 1 508 26.9 511 9 C 2 411.4 21.5 423 9 C 3 401.4 20.6 390 1

Result No.

Description

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RESULT 1 AW004482/c LOCUS DEFINITION

FEATURES

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/clone lib="A. thaliana, Columbia Col-0, rosette-3"
/note="vector: pSPORT; Site 1: Not!; Site 2: Sali; CDNA
library was derived from unireated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1::1, pear moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. CDNA synthesis was initiated
using a Not!-0igo(dT) primer. Double-stranded cDNA was
blunted, ligated to Sali adaptors, digested with Not!,
size-selected, and cloned into the Not! and Sali sites of
the pSPORT vector."
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  Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
Nobriga,A., Murry,L., Turner,C., Krikorian,S., Blder,L. and
                                                                    Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-273
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99.5%; Pred. No. 6.1e-68;
ive 0; Mismatches 2;
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412; Conservative
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AV808362/c
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 423)
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillhan, J., Guegler, K., Kin, C., Doyle, M., Brzoska, P., Wang, C., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,
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                                                                                                                                                                                                                                                             obtained from a clone generated
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                                                                                               Query Match 26.9%; Score 508; DB 9; Length 51 Best Local Similarity 99.4%; Pred. No. 2.8e-86; Matches 508; Conservative 0; Mismatches 3; Indels
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Fax: 314-427-3324
Email: service@genomesystems.com.
                                                                               Location/Qualifiers
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AI999808.1 GI:5846713
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AUTHORS
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CB261894 390 bp mRNA linear EST 06-NOV-2003 83-E8862-008-010-K04-pB12 MPIZ-ADIS-008 Arabidopsis thaliana CDNA clone MFIZp767K0410Q 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Burabana (Marabidopsis thaliana Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eustaryota; Viridiplantae, Streptophyta; Germatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases I to 390) T. S., Stracke, R., Torjek, O., Altmann, T., Mitchell.olds, T. and Weisshaar, B. Mitchell.olds, T. and Weisshaar, B. Larges-scale identification and analysis of genome-wide single-rucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
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63 AACCATGTACGACTATCATTACGTATGTTATAAGTTGTATATACAACTCCTTTATCTTTG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Bmail: weisshaa@mpiz-koeln.mpg.de
Insert Length: 390 Std Brror: 0.00
Plate: 10 row: K column: 04
Seq primer: pBl2: GGTGGGCGGCTGTAG.
                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                               Large scale analysis of Arabidopsis full-length cDNA (2002b)
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koydadi, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-4359
Fax: 81-298-36-1006
Email: meski@rtc.riken.go.jp
An Arabidopsis full-length CDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhOI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) disested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web as the (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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                                                                Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
I deservational II; Brassicales; Erassicaceae; Arabidopsis.
I (bases 1 to 423)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_rype="mRNA"
/db xref="texon:3702"
/dbo="RRNA"
/dcv_stage="plants at various developmental stages from germination to mature seeds"
/lab host="bH10B"
/clone lib="RAFL9"
/note="Site_1: BamH1; Site_2: Sall; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10 hr) treatments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 cccrraccccaaacarrcccaaaacarcrrcraccraraccaacrecracaacaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TIGIGITITACCAACTITGIGATAATTAGGCAATTGCTACTATGATTGCCCAAAACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1614 GATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAGTCACATTCAACCCAACGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
                                               Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
    GI:19842347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 419; Conserv
    AV808362.1
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                                                                       ORGANISM
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JOURNAL
COMMENT
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KEYWORDS
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The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."	Query Match Best Local Similarity 69.9%; Pred. No. 1.2e-42; Matches 411; Conservative 0; Mismatches 159; Indels 18; Gaps 2;		Qy 1128 CCATCTCTGGATCTTCTTCAATGGTGGATGATGGTGATATAGTCATTGCGTAGATGAGAT 1187	Qy 1188 TCATACGGTATATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCGG 1247	186 CTTTGCTGTCAAAGGGTTTCTCGACTATATAAGGACTTGAGAGAGA	Db 246 TAITCTTTCCATGGGATCAAATTTTAACAGTTCATGGTCAGAGAGGGATTATC 305 Qy 1353 TCAAGAAACCTCTATGTTCCACCAGCATTGCCTTCTGAGCAGGGAAAAGAAAG	QY 1413 TCAGATTTGGAGACCTCAACGAGGTTTGCCTGAGAAATCTGTTTCGGTTCTACGGAATTG 1472 Db 1617	QY 1473 GAIGTICCAAAACTICCTICACCCITACCCGAAAGAITGGGAGAAACGICTTGTAGCTAT 1532 DD 423 GAIGTITCAGAAITICCTCCATCCGTATCCTAAAGAIGCAGAAAGATTACTIGCAAT 482	Qy 1533 ACGAAGTGGCTTGACAAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCT 1592	OY 1593 ATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAA 1640 	-		KEFEKENCE I (Gases I TO 535) AUTHORS Town, C.D. Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. AUTHORS TOWN, C.D. Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. TITLE Whole genome shotgun sequencing of Brassica oleracea JOURNAL Unpublished (2001) COMMENT Other GSSe: BOGNT97TR CONTECT: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
	1616 TGTATGCGGAAATGAAGAAGCTCAATAACAGTCACATTCAACCCAACGGACGAAAAGAAAAGAAAAGAAAAAGAAAAAA	161 LETRIGGGGRAN GRANDAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AACCTAAA AACCTAAA	Oy 1796 CCATGTACGACTATCATTACGTATGTTATA 1825 	RESULT 5 CA117399 LOCUS CA917399 773 bp mRNA linear EST 27-DEC-2002 DEFINITION EST641546 GPOD Medicago truncatula cDNA clone GPOD-36E1, mRNA	sequence. CA917399 CA917399.1 EST. Medicago t	Σ	RS	TITLE More ESTs from developing reproductive tissues of Medicago truncatula JOURNAL Unpublished (2002) COMMENT Contact: Grusak, M.A.	DOM/ARS CHILDEN B NUCLICION RESEARCH CENTER BAYLOR College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713 798 7044 Fax: 713 798 7078	Email: mgrueak@bcm.tmc.edu TIGR sequence name: WT02025TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC). FEATURES 1773	/organism="Medicago truncatula" /mol_type="mRNR" /cultivar="A17" /db_xref="taxon:3880" /clone="0?00-36E1" /tissue_type="immature pod walls" /dev stage="immature pods, ranging in age from 15 to 30 /days_after_pollination"	/clone_11b="GFUO" / CLORE="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greehouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA.

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1439 IGCCIGAGAAATCIGITICGGITCIACGGAATTGGATGTICCAAAACTTCCTTCACCTT 1498
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                  F19 row: G column: 17.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGF19G17"
                                                                                                                                                                                                                                                       for details.
Plate: QGF19
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lettuce serriola Lactuca sativa cDNA clone
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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/mol type="genomic DNA"
factain="TO100DH3"
/db xref="teaxon:3712"
/clone="BGGNT87"
/clone="BGGNT87"
/note="Wector: pH0S1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PH0S1 using BstXI linkers"
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                                                                                                   Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.6%; Score 274.8; DB 28; Length
Best Local Similarity 85.7%; Pred. No. 4.5e-42;
Matches 317; Conservative 0; Mismatches 52; Indels
Tel: 301-838-3523
Emax: 301-838-0202
Email: cdrowndeigr.org
DNA is from a doubled haploid provided by
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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QGF19G17.yg.abl QG_EFGHJ le
QGF19G17, mRNA sequence.
BQ990079
BQ990079.1 GI:22409614
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AUTHORS
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/Jab host="More Total" |
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/Jab host="More Total" |
/Jab host="More Total" |
/Jab host="More Total" |
/Jab host="Westor: pBRcDMASfiab; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5° and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_INBEG_ERGNATIONERS pre-fertilized TAG_ERGG_ERGNATIONERS pre-fertilized TAG_ERGG_ERGNATIONERS pre-fertilized TAG_ERG_EGGTTGAACGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1379 ATTGCCTTCTTCAGCAGCTGAAACGAAAGCATCCAGATTTGGAGACCTCAACGAGGTT 1438
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Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
11. 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.crg [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4128, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1082 GTTTCGGATCTACATTTCAAAGGAGGCATTAGAAGCAAAGAAACCCATCTTTGGATC
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1192

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and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, and Shinozaki, sexi brobists sexi mercaki sexi plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan 7-1: 804dai, Shinozaki 4-1: 198-16-1960 Email: meski@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and Khol was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web as the (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV800635 AV80635 RAFL9 Arabidopsis thaliana CDNA clone RAFL09-24-021 3', RNA sequence. AV800635 AV80635 AV80635 AV80635
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Sosids, eurosida II, Brassicales; Brassicaceae, Arabidopsis.

(bases I to 270)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Arakawa,T., Shabata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.,
and Shinozaki,K.,
331 AGGTTTTGATCAAAGACGAGCATTAGAAGCAAAGAAAACCCAGCTCTTGGATCTTCTTCA 390
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/lab_host="DH10B"
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/note="Site_1: BamH1; Site_2: Sal1; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10,
                                                                                                                                                    .133 TCTTGGATCTTCTTCAAATGGTGGATGATCGATATAGTCATTGCGTAGATGAGATTCATA
                                                                                                                                                                                                 451 GAGTTGCGATTTGTCTTCAGGTGGATGATAAATATAGTCATTGCGTTGACGAGATTCATA
                                                                                                                                                                                                                                                       CGGTTATATCAGCGTTCCATGCTGCAACCGAGTTAGATCCACAGTTACACACCCGGTTTG
                                                                                                                                                                                                                                                                                                     571 CACTOCAAACCATCTCGTTCCTATACAAGAACCTGAGGGAGGAGAATCAGCAAAAGATAC
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                                                                                                391 AATGGTATATTCACACATATTATACATAAGATGGAGAATGATTTTGTTTTAAGTTTTT
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/db_xref="taxon:3702"
/clone="RAFL09-24-021"
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AV800635/c
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                                                                                                                                                                            BZ033022 719 bp DNA linear GSS 09-OCT-2002 och45h05.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"

/db_xref="taxon:3712"
/db_xref="taxon:3712"
/db_xref="taxon:3712"
/db_xref="taxon:3712"
/db_xref="taxon:3712"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shorgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeh45 row: h column: 05
Seq primer: -21UPpOT forward
Class: shorgun
T.A.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheoj
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Pred. No. 1.3e-38;
0; Mismatches 156; Indels 76;
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High quality sequence stop: 551.
Location/Qualifiers
1619 ATGCGGAAATGAACAAGAGGAAG 1641
                                                600 ACTTAGAGATGAATAGGAGGAGG 622
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al Similarity 66.3%;
456; Conservative 0
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Similarity Best Local Sim Matches 343; 1154 1274 1391 1451 1571 421 481 Query Match VERSION KEYWORDS SOURCE ORGANISM BZ031456/c LOCUS ACCESSION AUTHORS REFERENCE RESULT 11 ORIGIN ò g à g ò g ઠ g ò g ò g ò g ò d ò g accentuals, companiatus; Ascerates; Asceraceae; Cichoriondeae; Cichorieae; Lactuca.

I (bases 1 to 676)

S Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Elttuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
I Ungublished (2002)
Ungublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QC.A.Contig4128, see http://cgpdb.ucdavis.edu/ BU011811 67_EFGHJ lettuce serriola Lactuca sativa CDNA clone QGJ17D24.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa CDNA clone Ä 1587 TAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAA 1646 1647 TAACAGICACAITCAACCCAACGGACCAACTGTTCGAATGCCAAAAICTGITATGATGAG 1706 1707 CCAAGCAATGCATAAATAAGACAACAATTGTGTTTACCAACTTTGTGATAA-TTAGGCAA 1765 TTGCTACTCTATGATTGCCCAAAACCTAAACCATGTACGACTATCATTACGTATGTTATA 1825 211 Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorloideae; 210 TAACAGTCACATTCAACCCCACGGACCAACTCTTCGAATGCCCAAATCTGTTATGATGAG 151 CCAAGCCATGCATAAATAAGACAACAATTGTGTTTTACCCACTTTGTGATAATTTAGGCAAA 91 /lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each 31 TTGCTACTCTATGATTGCCCAAAACCTAAACCATGTACGACTATCATTACGTATGTTATA 270 TAGGCTATGGAAGCCGATGATAGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAA Gaps 1; Length 270; Indels 4. DB 9; 13.3%; Score 251.6; DB 9. 98.1%; Pred. No. 1.4e-37; iive 0; Mismatches 4. 1. .676 /organism="Lactuca sativa" /mol_type="mRNA" /cultivar="L.serriola" /db_xref="taxon:4236" /clone="QGJ17D24" Plate: QGJ17 row: D column: 24. Location/Qualifiers treatments" BU011811 BU011811.1 GI:22446206 EST. Conservative Lactuca sativa hr) Best Local Similarity Matches 265; Conserv 150 1766 90 Query Match ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS RESULT 10 BU011811 JOURNAL COMMENT REFERENCE AUTHORS FEATURES TITLE ORIGIN Q ò a ò 엄 ò g ò g

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source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_IIS=OG EFGHJ lettuce serriola
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BZ031456
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Brassica oleracea
Burassica oleracea
Buraryca, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 709)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Umpublished (2002)
Contact: Richard K. Wilson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AGCAGCTAAGAAGAAAAGATCATCATCAGCTATGGAGGCCGCAAAGAGGGCTTCCGGAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IGGAIGAGCGGIATAATCAGTGTTTAGATGAGATACATACGGTGATATCGGCATTTCACG
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                                                                                                                                                                                                                                                                                                               12.9%; Score 243; DB 13; Length 676;
.larity 69.9%; Pred. No. 4.5e-36;
Conservative 0; Mismatches 145; Indels 3
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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JOURNAL
COMMENT
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linear EST 16-OCT-2002
Populus tremula x Populus
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                                                                                                                                                                                                                                                            1 (bases 1 to 751)
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
Unneberg, P. halerao, R.R., Jansson, S. and Sterky, F.
He poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
                                                                                                                                                        Populus tremula x Populus tremuloides Populus tremula x Populus tremula x Populus tremuloides Bukaryota; Viridiplantea Streptoophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudioctyledons; core eudiocts; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGATGATCGATATAGTCATTGCGTAGATGAGATTCATACGGTTATATCAGCGTTCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 216.4; DB 13;
Pred. No. 4.8e-31;
0; Mismatches 136;
                                      BU837920 751 bp mRNA T107B12 Populus apical shoot cDNA library tremuloides cDNA 5 prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Umea Plant Science Center
Department of Plant Physiology
Unversity of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"

db_xref="teaxon:47664"

tissue_type="apical shoot"

/clore_lib="Populus apical shoot
                                                                                                                      GI:24020716
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68.8%;
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RESULT 12
BU837920
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                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 222.4; DB 28; Length 709;
.larity 69.0%; Pred. No. 3.5e-32;
Conservative 0; Mismatches 86; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                              132;
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column: 09
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Seq primer: -28RPpOT reverse
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High quality sequence stop: 551,
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Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots;

asterids; campanulis; Asterales; Asteracae; Asteroideae;

Heliantheae; Helianthus.

Is (Asess It of 672)

Kozik, Mithelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Inn, H., van Damme, M., Lavelle, D., Chevalier, R. Endford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compagnomics.ucdavis.edu/

Lupublished (2002)

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fr. Asterile
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                                                                 BU024863 672 bp mRNA linear EST 23-AUG-2002 QHF6H21.yg.abl QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA clone QHF6H21, mRNA sequence.
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TAG_SEQ=GCTAGTCGGG"
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                                                                                                                                                                                                                                                                                         Helianthus annuus (common sunflower)
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Location/Qualifiers
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BU024863.1 GI:22460383
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698 bp mRNA linear EST 23-AUG-2002
OFGITLI3.yg.abl OH EFGHJ SUnflower RHA280 Helianthus annuus CDNA
GLODE (HGITLI3, mRNA sequence.
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1 (bases 1 to 698)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Elin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Elison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lettuce and Sunflower ESTS from the Compositae Genome Project Unpublished (2002)
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1548 AAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGAT 1607
                                           260 GAGAAGTCAGGTTTCAAACTGGTTTATAAATGCTAGAGTTCGGCTATGGAAGCCAATGGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contacts Alexander Kozik (R.W.Michelmore)
Contacts Alexander Kozik (R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
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Tel: 1-(530)-742-1742
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Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2963, see http://cgpdb.ucdavis.edu/
for details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ACAAAGAGATTGCCGGAACGCTCTGTTTCGGTTCTTCGTGCTTGGCTGTTTGAACACTT
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                                                                                             AGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAG 1652
                                                                                                                                        320 AGAAGAGATGTACTTGGAAGAATGCAAGGAACATGAACAGAACAG 364
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                                                                                                                                                                                                                                                                                                                                                                                                           Helianthus annuus (common sunflower)
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/mol_type="genomic DNA"
/strain="Columbia on NA"
/strain="Columbia on NA"
/db_xref="taxon:3702"
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S Li,Y. Strizhov,N., Rosso,M. and Weisshaar,B.
Direct Submission
Direct Submission
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone 726P21.
The sequences are generated at the MPI for Plant Breeding Research
in the context of the GABI-Kat project. GABI-Kat is part of the
German Plant Genomics program designated 'GABI'. Information on
line availability can be found at:
http://www.mpiz.koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL946255 328 bp DNA linear GSS 24-OCT-2002 Arabidopsis thaliana T-DNA flanking sequence GK-295B12-015445,
                                                                                                                                                                             1548 AAGAAGTCAGGTATCAAACTGGTTTATAAATGCGCGGGTTAGGCTATGGAAGCCGATGAT 1607
1488 CCTTCACCCTTACCCGAAAGATTCGGAGAAACATCTTCTAGCTATACGAAGTGGCTTGAC 1547
                                                                          288 GAGAAGTCAGGTTTCAAACTGGTTTTATAAATGCTAGAGTTCGGCTATGGAAGCCAATGGT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
                                                                                                                                                                                                                                                                                                                                                          1608 AGAAGAGATGTATGCGGAAATGAACAAGAGGAAGCTCAATAACAG 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                         348 AGAAGAGATGTACTTGGAAGAATGCAAGGAACATGAACAGAACAG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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AL946255
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2; Gaps

7.7%; Score 146; DB 29; Length 328; 98.8%; Pred. No. 1.4e-17; Artive 0; Mismatches 0; Indels

Query Match Best Local Similarity 98.8¹ Matches 168; Conservative

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Db 25 CTGCGGAATGAAAGT-CACTGTTCTTTCACGGAGAAAGATAAATAACATTATCTTC 83

Oy 179 TTCTTCAGTTTTTAACACACATTTTGGAAATTTTGATGTAAAAATTCTCTTTGGAACGTT 238

Db 84 TTCTT-AGTTTTTTAACACACATTTTGGAAATTTTGATGTAAAATTCTCTTTGGAACGTT 142

Oy 239 GTGTTGTCTGAAATCTTCCCAAAGATTTTGATGTAAAAAATCTCTTTGGAACGTT 142

Db 143 GTGTTGTCTGAAATCTTCCCAAAGATTCTATCAGAAGAAAAAG 192

Search completed: September 2, 2004, 09:48:35

Job time: 4997 secs
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